GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 4, 2004, 10:56:28 ; Search time 192 Seconds
(without alignments)
961.954 Million cell updates/sec

Title: US-09-801-944B-268
Perfect score: 1661
Sequence: 1 MNQTLNSSGTVESALNYSRG.....EEPELEGGETPTVGTNEMGA 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1661	100.0	321	1	MRGD_HUMAN	Q8tds7 homo sapien
2	1661	100.0	321	2	AAR05120	Aar05120 homo sapi
3	1661	100.0	321	2	BAD20638	Bad20638 homo sapi
4	1439.5	86.7	320	1	MRGD_MACFA	Q61786 macaca fasc
5	1439.5	86.7	320	2	BAD20641	Bad20641 macaca fa
6	921.5	55.5	321	1	MRGD_MOUSE	Q91zb8 mus musculu
7	921.5	55.5	321	2	BAD20640	Bad20640 mus muscu
8	917.5	55.2	319	1	MRGD_RAT	Q7tn41 rattus norv
9	912.5	54.9	319	2	BAD20639	Bad20639 rattus no
10	548.5	33.0	322	1	MRG4_HUMAN	Q96la9 homo sapien
11	544.5	32.8	322	1	SNS5_HUMAN	Q8tdd7 homo sapien
12	542	32.6	322	1	SNS3_HUMAN	Q8tdd9 homo sapien
13	538.5	32.4	322	1	MRG1_HUMAN	Q96lb2 homo sapien
14	525	31.6	323	2	Q7TN42	Q7tn42 rattus norv
15	522	31.4	330	1	MRG2_HUMAN	Q96lb1 homo sapien
16	522	31.4	330	2	AAH63450	Aah63450 homo sapi
17	521	31.4	323	1	SNS1_RAT	Q8r4g1 rattus norv
18	518.5	31.2	322	2	Q8CIP3	Q8cip3 mus musculu
19	515.5	31.0	323	2	Q7TN45	Q7tn45 rattus norv
20	514	30.9	321	2	Q91ZC0	Q91zc0 mus musculu
21	510.5	30.7	322	2	AAH67292	Aah67292 homo sapi
22	508	30.6	302	1	MGA3_MOUSE	Q91ww3 mus musculu
23	506	30.5	322	1	MRG3_HUMAN	Q96lb0 homo sapien
24	503	30.3	304	1	MGA1_MOUSE	Q91ww5 mus musculu
25	499	30.0	304	1	MRGA_RAT	Q7tn49 rattus norv
26	499	30.0	331	2	Q91YB7	Q91yb7 rattus norv
27	494.5	29.8	313	1	MGA4_MOUSE	Q91ww2 mus musculu
28	493.5	29.7	305	1	MGA8_MOUSE	Q91zc4 mus musculu
29	492	29.6	294	2	Q7TN48	Q7tn48 rattus norv
30	492	29.6	322	1	SNS2_HUMAN	Q8tde0 homo sapien
31	488.5	29.4	321	2	Q99MT8	Q99mt8 mus musculu
32	484.5	29.2	310	2	Q711I9	Q711i9 mus musculu
33	484.5	29.2	310	2	Q91ZB7	Q91zb7 mus musculu
34	484.5	29.2	310	2	CAC86257	Cac86257 mus muscu
35	481.5	29.0	338	2	Q91ZC2	Q91zc2 mus musculu
36	481.5	29.0	343	1	MRGF_HUMAN	Q96am1 homo sapien
37	478	28.8	328	2	Q8IXE2	Q8ixe2 homo sapien
38	477.5	28.7	338	2	Q8CDY4	Q8cdy4 mus musculu
39	475	28.6	322	2	Q91ZB9	Q91zb9 mus musculu
40	474.5	28.6	321	2	Q7TN38	Q7tn38 rattus norv
41	473	28.5	338	2	Q91ZC3	Q91zc3 mus musculu
42	472.5	28.4	304	2	Q8N7J6	Q8n7j6 homo sapien
43	472.5	28.4	305	1	MGA7_MOUSE	Q91zc5 mus musculu
44	471.5	28.4	301	1	MGA6_MOUSE	Q91zc6 mus musculu
45	470.5	28.3	331	2	AAH64040	Aah64040 mus muscu

ALIGNMENTS

```
RESULT 1
MRGD_HUMAN
ID   MRGD_HUMAN     STANDARD;      PRT;   321 AA.
AC   Q8TDS7; Q8NGK7;
DT   01-OCT-2004 (Rel. 45, Created)
DT   01-OCT-2004 (Rel. 45, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Mas-related G-protein coupled receptor member D (Beta-alanine
DE   receptor) (G protein-coupled receptor TGR7).
GN   Name=MRGPRD; Synonyms=MRGD;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22810130; PubMed=12909716; DOI=10.1073/pnas.1732949100;
RA   Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;
RT   "Atypical expansion in mice of the sensory neuron-specific Mrg G
RT   protein-coupled receptor family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).
RN   [2]
RP   SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND POSSIBLE FUNCTION.
RC   TISSUE=Liver;
RX   PubMed=15037633; DOI=10.1074/jbc.M314240200;
RA   Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.,
RA   Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Watanabe T.,
RA   Moriya T., Itoh Y., Hinuma S.;
RT   "Identification of a G protein-coupled receptor specifically
RT   responsive to beta-alanine.";
RL   J. Biol. Chem. 279:23559-23564(2004).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22040266; PubMed=12044878;
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT   "Identification of G protein-coupled receptor genes from the human
RT   genome sequence.";
RL   FEBS Lett. 520:97-101(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May regulate nociceptor function and/or development,
CC       including the sensation or modulation of pain. Functions as a
CC       specific membrane receptor for beta-alanine. Beta-alanine at
CC       micromolar doses specifically evoked Ca(2+) influx in cells
CC       expressing the receptor. Beta-alanine decreases forskolin-
CC       stimulated cAMP production in cells expressing the receptor,
CC       suggesting that the receptor couples with G-protein G(q) and G(i).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Localized at the
CC       plasma membrane but internalized into the cytoplasm after
```

```
CC       treatment with beta-alanine.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC       Mas subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY427820; AAR05120.1; -.
DR   EMBL; AB154410; BAD20638.1; -.
DR   EMBL; AB083627; BAB89340.1; -.
DR   EMBL; AB065786; BAC06005.1; ALT_INIT.
DR   Genew; HGNC:29626; MRGPRD.
DR   MIM; 607231; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN        1     33       Extracellular (Potential).
FT   TRANSMEM     34     54       1 (Potential).
FT   DOMAIN       55     59       Cytoplasmic (Potential).
FT   TRANSMEM     60     80       2 (Potential).
FT   DOMAIN       81    112       Extracellular (Potential).
FT   TRANSMEM    113    133       3 (Potential).
FT   DOMAIN      134    142       Cytoplasmic (Potential).
FT   TRANSMEM    143    163       4 (Potential).
FT   DOMAIN      164    184       Extracellular (Potential).
FT   TRANSMEM    185    205       5 (Potential).
FT   DOMAIN      206    218       Cytoplasmic (Potential).
FT   TRANSMEM    219    239       6 (Potential).
FT   DOMAIN      240    257       Extracellular (Potential).
FT   TRANSMEM    258    280       7 (Potential).
FT   DOMAIN      281    321       Cytoplasmic (Potential).
FT   CARBOHYD      2      2       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD      6      6       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     16     16       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     92     92       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   321 AA;  36117 MW;  B45AB7FEB2154B40 CRC64;

  Query Match             100.0%;  Score 1661;  DB 1;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-117;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

```
RESULT 2
AAR05120
ID   AAR05120    PRELIMINARY;      PRT;   321 AA.
AC   AAR05120;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   G-protein coupled receptor.
GN   MRGD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22810130; PubMed=12909716;
RA   Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;
RT   "Atypical expansion in mice of the sensory neuron-specific Mrg G
RT   protein-coupled receptor family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).
DR   EMBL; AY427820; AAR05120.1; -.
KW   Receptor.
SQ   SEQUENCE   321 AA;  36117 MW;  B45AB7FEB2154B40 CRC64;

  Query Match             100.0%;  Score 1661;  DB 2;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-117;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

```
RESULT 3
BAD20638
ID   BAD20638    PRELIMINARY;      PRT;   321 AA.
AC   BAD20638;
DT   01-JUN-2004 (TrEMBLrel. 27, Created)
DT   01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein-coupled receptor TGR7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.,
RA   Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Watanabe T.,
RA   Moriya T., Itoh Y., Hinuma S.;
RT   "Identification of a G Protein-coupled Receptor Specifically
RT   Responsive to beta-Alanine.";
```

```
RL   J. Biol. Chem. 279:23559-23564(2004).
DR   EMBL; AB154410; BAD20638.1; -.
KW   Receptor.
SQ   SEQUENCE   321 AA;  36117 MW;  B45AB7FEB2154B40 CRC64;

  Query Match             100.0%;  Score 1661;  DB 2;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-117;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 4
MRGD_MACFA
ID   MRGD_MACFA     STANDARD;      PRT;   320 AA.
AC   Q6L786;
DT   01-OCT-2004 (Rel. 45, Created)
DT   01-OCT-2004 (Rel. 45, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Mas-related G-protein coupled receptor member D (Beta-alanine
DE   receptor) (G protein-coupled receptor TGR7).
GN   Name=MRGPRD; Synonyms=MRGD;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX   PubMed=15037633; DOI=10.1074/jbc.M314240200;
RA   Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.,
RA   Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Watanabe T.,
RA   Moriya T., Itoh Y., Hinuma S.;
RT   "Identification of G protein-coupled receptor genes from the human
RT   genome sequence.";
RL   J. Biol. Chem. 279:23559-23564(2004).
CC   -!- FUNCTION: May regulate nociceptor function and/or development,
CC       including the sensation or modulation of pain. Functions as a
CC       specific membrane receptor for beta-alanine. The receptor couples
CC       with G-protein G(q) and G(i) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Co-expressed in the small diameter neurons
CC       with P2X3 and VR1 in dorsal root ganglia.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC       Mas subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB154413; BAD20641.1; -.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN       1     33       Extracellular (Potential).
FT   TRANSMEM    34     54       1 (Potential).
FT   DOMAIN      55     62       Cytoplasmic (Potential).
FT   TRANSMEM    63     83       2 (Potential).
FT   DOMAIN      84    112       Extracellular (Potential).
FT   TRANSMEM   113    133       3 (Potential).
FT   DOMAIN     134    142       Cytoplasmic (Potential).
FT   TRANSMEM   143    163       4 (Potential).
FT   DOMAIN     164    182       Extracellular (Potential).
FT   TRANSMEM   183    203       5 (Potential).
FT   DOMAIN     204    218       Cytoplasmic (Potential).
FT   TRANSMEM   219    239       6 (Potential).
FT   DOMAIN     240    257       Extracellular (Potential).
FT   TRANSMEM   258    280       7 (Potential).
FT   DOMAIN     281    320       Cytoplasmic (Potential).
FT   CARBOHYD     2      2       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     6      6       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    16     16       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   320 AA;  35944 MW;  265E137FC7E5481C CRC64;

  Query Match             86.7%;  Score 1439.5;  DB 1;  Length 320;
  Best Local Similarity   88.2%;  Pred. No. 7.6e-101;
  Matches  283;  Conservative   13;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              |||||||||| | |||:|||| || | ||||||||||||||||||||||||||| | |
Db          1 MNQTLNSSGTAELALNHSRGSVVHAACLVLSSLAMFTCLCGMAGNSMVIWLLGFRMRRTP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              | ||||||||||||:| ||: ||||||||||:|||||||||||| ||||||||||||||
Db         61 FSIYILNLAAADLLFVFCMAAMLSLETQPLVSTTDKVHELMKRLKYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              |||||||||||||||||||||||| ||| |||| ||||| ||||||||||:|:|||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCALLWMLCLLTNGLTSCFCSKFLKFNKDQCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||  |
Db        181 VQAALIMGVLTPVMTLSSLTLFVRVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLGFY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              |||||||:|||: :|| |:|||||||:|||||:|||||||||| ||   |||||||:||
Db        241 WFVLYWLNLPPDTKVLYFNLSRLSSSMSSSANPLIYFLVGSRRSRRL-QGSLGTVLQRAL 299

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||| |||||||
Db        300 REEPELEGGETPTTGTNEMGA 320


RESULT 5
BAD20641
ID   BAD20641    PRELIMINARY;      PRT;   320 AA.
AC   BAD20641;
DT   01-JUN-2004 (TrEMBLrel. 27, Created)
DT   01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein-coupled receptor TGR7.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.,
RA   Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Watanabe T.,
```

```
RA   Moriya T., Itoh Y., Hinuma S.;
RT   "Identification of a G Protein-coupled Receptor Specifically
RT   Responsive to beta-Alanine.";
RL   J. Biol. Chem. 279:23559-23564(2004).
DR   EMBL; AB154413; BAD20641.1; -.
KW   Receptor.
SQ   SEQUENCE   320 AA;  35944 MW;  265E137FC7E5481C CRC64;

  Query Match             86.7%;  Score 1439.5;  DB 2;  Length 320;
  Best Local Similarity   88.2%;  Pred. No. 7.6e-101;
  Matches  283;  Conservative   13;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              |||||||||| | |||:|||| || | |||||||||||||||||||||||||||| | |
Db          1 MNQTLNSSGTAELALNHSRGSVVHAACLVLSSLAMFTCLCGMAGNSMVIWLLGFRMRRTP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              | |||||||||||||:| ||: |||||||||:|||||||||||| ||||||||||||||
Db         61 FSIYILNLAAADLLFVFCMAAMLSLETQPLVSTTDKVHELMKRLKYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              |||||||||||||||||||||||| ||| |||| |||| |||||||||:|:||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCALLWMLCLLTNGLTSCFCSKFLKFNKDQCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||| |
Db        181 VQAALIMGVLTPVMTLSSLTLFVRVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLGFY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              |||||||:|||: :|| |:|||||||:||||||:|||||||||| ||   |||||||:||
Db        241 WFVLYWLNLPPDTKVLYFNLSRLSSSMSSSANPLIYFLVGSRRSRRL-QGSLGTVLQRAL 299

Qy        301 REEPELEGGETPTVGTNEMGA 321
              ||||||||||||| |||||||
Db        300 REEPELEGGETPTTGTNEMGA 320


RESULT 6
MRGD_MOUSE
ID   MRGD_MOUSE     STANDARD;      PRT;   321 AA.
AC   Q91ZB8;
DT   01-OCT-2004 (Rel. 45, Created)
DT   01-OCT-2004 (Rel. 45, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Mas-related G-protein coupled receptor member D (Beta-alanine
DE   receptor) (G protein-coupled receptor TGR7).
GN   Name=Mrgprd; Synonyms=Mrgd;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC   STRAIN=C57BL/6;
RX   MEDLINE=21435808; PubMed=11551509;
RA   Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT   "A diverse family of GPCRs expressed in specific subsets of
RT   nociceptive sensory neurons.";
RL   Cell 106:619-632(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   PubMed=15037633; DOI=10.1074/jbc.M314240200;
RA   Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.,
RA   Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Watanabe T.,
RA   Moriya T., Itoh Y., Hinuma S.;
RT   "Identification of a G protein-coupled receptor specifically
RT   responsive to beta-alanine.";
RL   J. Biol. Chem. 279:23559-23564(2004).
CC   -!- FUNCTION: May regulate nociceptor function and/or development,
CC       including the sensation or modulation of pain. Functions as a
CC       specific membrane receptor for beta-alanine. The receptor couples
CC       with G-protein G(q) and G(i) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that
CC       includes nociceptors. Expressed in the subclass of nonpeptidergic
CC       sensory neurons that are IB4(+) and VR1(-).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC       Mas subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY042209; AAK91800.1; -.
DR   EMBL; AB154412; BAD20640.1; -.
DR   MGD; MGI:3033142; Mrgprd.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN       1      8       Extracellular (Potential).
FT   TRANSMEM     9     29       1 (Potential).
FT   DOMAIN      30     30       Cytoplasmic (Potential).
FT   TRANSMEM    31     51       2 (Potential).
FT   DOMAIN      52     72       Extracellular (Potential).
FT   TRANSMEM    73     93       3 (Potential).
FT   DOMAIN      94    146       Cytoplasmic (Potential).
FT   TRANSMEM   147    167       4 (Potential).
FT   DOMAIN     168    181       Extracellular (Potential).
FT   TRANSMEM   182    202       5 (Potential).
FT   DOMAIN     203    220       Cytoplasmic (Potential).
FT   TRANSMEM   221    241       6 (Potential).
FT   DOMAIN     242    260       Extracellular (Potential).
FT   TRANSMEM   261    281       7 (Potential).
FT   DOMAIN     282    321       Cytoplasmic (Potential).
FT   CARBOHYD     2      2       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   321 AA;  36125 MW;  B0642547A75077B3 CRC64;

  Query Match             55.5%;  Score 921.5;  DB 1;  Length 321;
  Best Local Similarity   58.5%;  Pred. No. 1.1e-61;
  Matches  190;  Conservative   49;  Mismatches   73;  Indels   13;  Gaps    5;

Qy          1 MNQTLNSSG----TVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFR- 55
              || ||:||     |:   ::      |   | :: ||| ||: ||||||:|||||
Db          1 MNSTLDSSPAPGLTISPTMD-----LVTWIYFSVTFLAMATCVGGMAGNSLVIWLLSCNG 55

Qy         56 MHRNPFCIYILNLAAADLLFLFSMASTLSLETQPL--VNTTDKVHELMKRLMYFAYTVGL 113
              | |:|||:|:|||| || |||| ||| ||||| ||   || : |::| |:|: ||||| ||
Db         56 MQRSPFCVYVLNLAVADFLFLFCMASMLSLETGPLLIVNISAKIYEGMRRIKYFAYTAGL 115

Qy        114 SLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNED 173
              |||||||||||||||||:|||||||||: | | || |  ||| | | || :|   |:
Db        116 SLLTAISTQRCLSVLFPIWYKCHRPRHLSSVVSGALWALAFLMNFLASFFCVQFWHPNKH 175

Qy        174 RCFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLIC 233
              :||:||:|  :||:|:  ||| |:|  ||: ||::|   ||:| ||:||:| |:|||| |
Db        176 QCFKVDIVFNSLILGIFMPVMILTSTILFIRVRKNSLMQRRRPRRLYVVILTSILVFLTC 235

Qy        234 SLPLSIYWFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLG 293
              |||| | ||:|||: :  ::::|   :|| |||:|||||||||||::|||   |||
Db        236 SLPLGINWFLLYWVDVKRDVRLLYSCVSRFSSSLSSSANPVIYFLVGSQKSHRL-QESLG 294

Qy        294 TVLQQALREEPELEGGETPTVGTNE 318
              || :|||:||| || |||:  ||:
Db        295 AVLGRALRDEPEPEGRETPSTCTND 319


RESULT 7
BAD20640
ID   BAD20640    PRELIMINARY;      PRT;   321 AA.
```

```
AC   BAD20640;
DT   01-JUN-2004 (TrEMBLrel. 27, Created)
DT   01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein-coupled receptor TGR7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.,
RA   Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Watanabe T.,
RA   Moriya T., Itoh Y., Hinuma S.;
RT   "Identification of a G Protein-coupled Receptor Specifically
RT   Responsive to beta-Alanine.";
RL   J. Biol. Chem. 279:23559-23564(2004).
DR   EMBL; AB154412; BAD20640.1; -.
KW   Receptor.
SQ   SEQUENCE   321 AA;  36125 MW;  B0642547A75077B3 CRC64;

  Query Match             55.5%;  Score 921.5;  DB 2;  Length 321;
  Best Local Similarity   58.5%;  Pred. No. 1.1e-61;
  Matches  190;  Conservative   49;  Mismatches   73;  Indels   13;  Gaps    5;

Qy          1 MNQTLNSSG----TVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFR- 55
              || ||:||      |:   ::      |   | :: ||| ||: ||||||:|||||
Db          1 MNSTLDSSPAPGLTISPTMD-----LVTWIYFSVTFLAMATCVGGMAGNSLVIWLLSCNG 55

Qy         56 MHRNPFCIYILNLAAADLLFLFSMASTLSLETQPL--VNTTDKVHELMKRLMYFAYTVGL 113
              | |:|||:|:|||| || |||| ||| |||||  ||  || : |::| |:|: |||||
Db         56 MQRSPFCVYVLNLAVADFLFLFCMASMLSLETGPLLIVNISAKIYEGMRRIKYFAYTAGL 115

Qy        114 SLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNED 173
              ||||||||||||||||||:|||||||||: | | || |  ||| | | || :|   |:
Db        116 SLLTAISTQRCLSVLFPIWYKCHRPRHLSSVVSGALWALAFLMNFLASFFCVQFWHPNKH 175

Qy        174 RCFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLIC 233
              :||:||:|  :||:|:  ||| |:|  ||: ||::|   ||:| ||:||:| |:|||| |
Db        176 QCFKVDIVFNSLILGIFMPVMILTSTILFIRVRKNSLMQRRRPRRLYVVILTSILVFLTC 235

Qy        234 SLPLSIYWFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLG 293
              |||| | ||:|||: :  ::::|   :|| |||:||||||||||||::||||   |||
Db        236 SLPLGINWFLLYWVDVKRDVRLLYSCVSRFSSSLSSSANPVIYFLVGSQKSHRL-QESLG 294

Qy        294 TVLQQALREEPELEGGETPTVGTNE 318
              || :|||:||| || |||:  ||:
Db        295 AVLGRALRDEPEPEGRETPSTCTND 319


RESULT 8
MRGD_RAT
ID   MRGD_RAT       STANDARD;      PRT;   319 AA.
AC   Q7TN41; Q6L788;
DT   01-OCT-2004 (Rel. 45, Created)
DT   01-OCT-2004 (Rel. 45, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Mas-related G-protein coupled receptor member D (Beta-alanine
DE   receptor) (G protein-coupled receptor TGR7).
GN   Name=Mrgprd; Synonyms=Mrgd;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=22810130; PubMed=12909716; DOI=10.1073/pnas.1732949100;
RA   Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;
RT   "Atypical expansion in mice of the sensory neuron-specific Mrg G
RT   protein-coupled receptor family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).
RN   [2]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC   TISSUE=Cerebellum;
RX   PubMed=15037633; DOI=10.1074/jbc.M314240200;
RA   Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.,
RA   Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Watanabe T.,
RA   Moriya T., Itoh Y., Hinuma S.;
RT   "Identification of a G protein-coupled receptor specifically
RT   responsive to beta-alanine.";
RL   J. Biol. Chem. 279:23559-23564(2004).
CC   -!- FUNCTION: May regulate nociceptor function and/or development,
CC       including the sensation or modulation of pain. Functions as a
CC       specific membrane receptor for beta-alanine. The receptor couples
CC       with G-protein G(q) and G(i) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Co-expressed in the small diameter neurons
CC       with P2X3 and VR1 in dorsal root ganglia.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC       Mas subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF518246; AAQ08318.1; -.
DR   EMBL; AB154411; BAD20639.1; -.
DR   RGD; 738040; Mrgprd.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane.
FT   DOMAIN       1     30       Extracellular (Potential).
FT   TRANSMEM     31    51       1 (Potential).
FT   DOMAIN       52    64       Cytoplasmic (Potential).
FT   TRANSMEM     65    85       2 (Potential).
FT   DOMAIN       86    92       Extracellular (Potential).
FT   TRANSMEM     93    113      3 (Potential).
FT   DOMAIN       114   144      Cytoplasmic (Potential).
FT   TRANSMEM     145   165      4 (Potential).
FT   DOMAIN       166   184      Extracellular (Potential).
FT   TRANSMEM     185   205      5 (Potential).
FT   DOMAIN       206   220      Cytoplasmic (Potential).
FT   TRANSMEM     221   241      6 (Potential).
FT   DOMAIN       242   260      Extracellular (Potential).
FT   TRANSMEM     261   281      7 (Potential).
FT   DOMAIN       282   319      Cytoplasmic (Potential).
FT   CONFLICT     55    55       R -> S (in Ref. 2).
SQ   SEQUENCE   319 AA;  35830 MW;  500F41492DE002F7 CRC64;

  Query Match             55.2%;  Score 917.5;  DB 1;  Length 319;
  Best Local Similarity   58.8%;  Pred. No. 2.1e-61;
  Matches  191;  Conservative   48;  Mismatches   71;  Indels   15;  Gaps    6;

Qy          1 MNQTLNSSG----TVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGF-R 55
              || |  ||     |:   ::      |   | :: ||| ||:||: ||||||||| | |
Db          1 MNYTPYSSPAPGLTISPTMD-----PVTWVYFSVTFLAMATCVCGIVGNSMVIWLLSFHR 55

Qy         56 MHRNPFCIYILNLAAADLLFLFSMASTLSLETQPLV--NTTDKVHELMKRLMYFAYTVGL 113
              : |:||| |:|||| ||||||  ||| ||||| ||:  :|: :|:| |||: ||||| ||
Db         56 VQRSPFCTYVLNLAVADLLFLLCMASLLSLETGPLLTASTSARVYEGMKRIKYFAYTAGL 115

Qy        114 SLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNED 173
              |||||||||||||||||:|||||:|||   |||:|| | |||| | | || :|   ::
Db        116 SLLTAISTQRCLSVLFPIWYKCHRPQHLSGVVCGVLWALALLMNFLASFFCVQFWHPDKY 175

Qy        174 RCFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLIC 233
              :||:|||  :||:|:  ||| |:|  :|: :|::|   |||| ||:||:| |||||| |
Db        176 QCFKVDMVFNSLILGIFMPVMVLTSAIIFIRMRKNSLLQRRQPRRLYVVILTSVLVFLTC 235
```

```
Qy        234 SLPLSIYWFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLG 293
              |||| | ||:|||: ||  :::|    || |||:||||||||||||::||||   |||
Db        236 SLPLGINWFLLYWVELPQAVRLLYVCSSRFSSSLSSSANPVIYFLVGSQKSHRL-QESLG 294

Qy        294 TVLQQALREEPELEGGETPTVGTNE 318
                || :||::||  || |||:  ||:
Db        295 AVLGRALQDEP--EGRETPSTCTND 317


RESULT 9
BAD20639
ID   BAD20639    PRELIMINARY;      PRT;   319 AA.
AC   BAD20639;
DT   01-JUN-2004 (TrEMBLrel. 27, Created)
DT   01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein-coupled receptor TGR7.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shinohara T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H.,
RA   Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Watanabe T.,
RA   Moriya T., Itoh Y., Hinuma S.;
RT   "Identification of a G Protein-coupled Receptor Specifically
RT   Responsive to beta-Alanine.";
RL   J. Biol. Chem. 279:23559-23564(2004).
DR   EMBL; AB154411; BAD20639.1; -.
KW   Receptor.
SQ   SEQUENCE   319 AA;  35761 MW;  505A50492D7E72F7 CRC64;

  Query Match             54.9%;  Score 912.5;  DB 2;  Length 319;
  Best Local Similarity   58.5%;  Pred. No. 5.1e-61;
  Matches  190;  Conservative   48;  Mismatches   72;  Indels   15;  Gaps    6;

Qy          1 MNQTLNSSG----TVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFR- 55
              || |  ||     |:   ::      |   |  :: ||| ||:||: |||||||| |
Db          1 MNYTPYSSPAPGLTISPTMD-----PVTWVYFSVTFLAMATCVCGIVGNSMVIWLLSFHS 55

Qy         56 MHRNPFCIYILNLAAADLLLFLFSMASTLSLETQPLV--NTTDKVHELMKRLMYFAYTVGL 113
              : |:||| |:|||| ||||||  ||| ||||| ||:  :|: :|:| ||| : ||||| ||
Db         56 VQRSPFCTYVLNLAVADLLLFLLCMASLLSLETGPLLTASTSARVYEGMKRIKYFAYTAGL 115

Qy        114 SLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNED 173
              |||||||||||||||||||:||||:|||  |||:|| | |||| | | || :|   ::
Db        116 SLLTAISTQRCLSVLFPIWYKCHRPQHLSGVVCGVLWALALLMNFLASFFCVQFWHPDKY 175

Qy        174 RCFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLIC 233
              :||:|||  :||:|:  ||| |:|  :|: :|::|   |||| ||:||:| |||||| |
Db        176 QCFKVDMVFNSLILGIFMPVMVLTSAIIFIRMRKNSLLQRRQPRRLYVVILTSVLVFLTC 235

Qy        234 SLPLSIYWFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLG 293
              |||| | ||:|||: ||  :::|    || |||:||||||||||||::||||   |||
Db        236 SLPLGINWFLLYWVELPQAVRLLYVCSSRFSSSLSSSANPVIYFLVGSQKSHRL-QESLG 294

Qy        294 TVLQQALREEPELEGGETPTVGTNE 318
                || :||::||  || |||:  ||:
Db        295 AVLGRALQDEP--EGRETPSTCTND 317


RESULT 10
MRG4_HUMAN
ID   MRG4_HUMAN     STANDARD;      PRT;   322 AA.
AC   Q96LA9; Q8TDD6;
DT   01-OCT-2004 (Rel. 45, Created)
DT   01-OCT-2004 (Rel. 45, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Mas-related G-protein coupled receptor member X4 (Sensory neuron-
DE   specific G-protein coupled receptor 6).
GN   Name=MRGX4; Synonyms=SNSR6;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21435808; PubMed=11551509;
RA   Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT   "A diverse family of GPCRs expressed in specific subsets of
RT   nociceptive sensory neurons.";
RL   Cell 106:619-632(2001).
RN   [2]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX   MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nn815;
RA   Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA   Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA   Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,
RA   Dray A., Walker P., Ahmad S.;
RT   "Proenkephalin A gene products activate a new family of sensory
RT   neuron-specific GPCRs.";
RL   Nat. Neurosci. 5:201-209(2002).
CC   -!- FUNCTION: Orphan receptor. Probably involved in the function of
CC       nociceptive neurons. May regulate nociceptor function and/or
CC       development, including the sensation or modulation of pain.
CC       Potently activated by enkephalins (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
CC       root and trigeminal sensory neurons.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC       Mas subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY042216; AAK91807.1; -.
DR   EMBL; AF474992; AAL86883.1; -.
DR   MIM; 607230; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
FT   DOMAIN        1     31       Extracellular (Potential).
FT   TRANSMEM     32     52       1 (Potential).
FT   DOMAIN       53     60       Cytoplasmic (Potential).
FT   TRANSMEM     61     81       2 (Potential).
FT   DOMAIN       82     96       Extracellular (Potential).
FT   TRANSMEM     97    117       3 (Potential).
FT   DOMAIN      118    137       Cytoplasmic (Potential).
FT   TRANSMEM    138    158       4 (Potential).
FT   DOMAIN      159    177       Extracellular (Potential).
FT   TRANSMEM    178    198       5 (Potential).
FT   DOMAIN      199    218       Cytoplasmic (Potential).
FT   TRANSMEM    219    239       6 (Potential).
FT   DOMAIN      240    254       Extracellular (Potential).
FT   TRANSMEM    255    275       7 (Potential).
FT   DOMAIN      276    322       Cytoplasmic (Potential).
FT   CARBOHYD     25     25       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     89     89       N-linked (GlcNAc. . .) (Potential).
FT   VARIANT       8      8       F -> L (in dbSNP:2468774).
FT                                 /FTId=VAR_019435.
FT   VARIANT      25     25       N -> K (in dbSNP:2445180).
FT                                 /FTId=VAR_019436.
FT   VARIANT      54     54       Y -> C (in dbSNP:1869788).
FT                                 /FTId=VAR_019437.
FT   VARIANT      83     83       S -> L (in dbSNP:2445179).
FT                                 /FTId=VAR_019438.
FT   CONFLICT    182    182       A -> V (in Ref. 2).
```

```
FT   CONFLICT    319    319       R -> K (in Ref. 2).
SQ   SEQUENCE   322 AA;  36434 MW;  7CA676F8BD390A31 CRC64;

  Query Match             33.0%;  Score 548.5;  DB 1;  Length 322;
  Best Local Similarity   42.2%;  Pred. No. 1.7e-33;
  Matches  135;  Conservative   56;  Mismatches  104;  Indels   25;  Gaps   10;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              |: |:   ||  : :|    :  :   |  : |      | |: ||::|:||||:|| ||
Db          1 MDPTVPVFGTKLTPINGREETPCYNQTLSFTVLTCIISLVGLTGNAVVLWLLGYRMRRNA 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQP--LVNTTDKVHELMKRLMYFAYTVGLSLLTA 118
               |||||||||| |||     :  :   |  |:| :  : :::  :| | | |||:|:|
Db         61 VSIYILNLAAADFLFL-----SFQIIRSPLRLINISHLIRKILVSVMTFPYFTGLSMLSA 115

Qy        119 ISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR--CF 176
              |||:||||||:|||::| || |||| || ||| | || : |   ||  ||    |   |
Db        116 ISTERCLSVLWPIWYRCRRPTHLSAVVCVLLWGLSLLFSMLEWRFCD-FLFSGADSSWCE 174

Qy        177 RVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLVFLICSL 235
                | :  | ::  |  |: :||| | | :   |   |: | |||:| :| :|||||:| |
Db        175 TSDFIPVAWLI-FLCVVLCVSSLVLLVRILCGS---RKMPLTRLYVTILLTVLVFLLCGL 230

Qy        236 PLSIYWFVLYWLSLPPE-----MQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTR 290
              |  |   ::| : |   |     : ::| ||     ||::|||||:||| ||| |  |   :
Db        231 PFGILGALIYRMHLNLEVLYCHVYLVCMSL----SSLNSSANPIIYFFVGSFR-QRQNRQ 285

Qy        291 SLGTVLQQALREEPELEGGE 310
              :|  |||:||:::||:: ||
Db        286 NLKLVLQRALQDKPEVDKGE 305


RESULT 11
SNS5_HUMAN
ID   SNS5_HUMAN     STANDARD;      PRT;   322 AA.
AC   Q8TDD7;
DT   01-OCT-2004 (Rel. 45, Created)
DT   01-OCT-2004 (Rel. 45, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sensory neuron-specific G-protein coupled receptor 5.
GN   Name=SNSR5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX   MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nn815;
RA   Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA   Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA   Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,
RA   Dray A., Walker P., Ahmad S.;
RT   "Proenkephalin A gene products activate a new family of sensory
RT   neuron-specific GPCRs.";
RL   Nat. Neurosci. 5:201-209(2002).
CC   -!- FUNCTION: Orphan receptor. Probably involved in the function of
CC       nociceptive neurons. May regulate nociceptor function and/or
CC       development, including the sensation or modulation of pain.
CC       Potently activated by enkephalins (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
CC       root and trigeminal sensory neurons.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC       Mas subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF474991; AAL86882.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane.
FT   DOMAIN        1     31       Extracellular (Potential).
FT   TRANSMEM     32     52       1 (Potential).
FT   DOMAIN       53     60       Cytoplasmic (Potential).
FT   TRANSMEM     61     81       2 (Potential).
FT   DOMAIN       82     96       Extracellular (Potential).
FT   TRANSMEM     97    117       3 (Potential).
FT   DOMAIN      118    137       Cytoplasmic (Potential).
FT   TRANSMEM    138    158       4 (Potential).
FT   DOMAIN      159    177       Extracellular (Potential).
FT   TRANSMEM    178    198       5 (Potential).
FT   DOMAIN      199    218       Cytoplasmic (Potential).
FT   TRANSMEM    219    239       6 (Potential).
FT   DOMAIN      240    254       Extracellular (Potential).
FT   TRANSMEM    255    275       7 (Potential).
FT   DOMAIN      276    322       Cytoplasmic (Potential).
FT   CARBOHYD     89     89       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   322 AA;  36423 MW;  3D6FFB4B5DDFDD90 CRC64;

  Query Match             32.8%;  Score 544.5;  DB 1;  Length 322;
  Best Local Similarity   42.7%;  Pred. No. 3.4e-33;
  Matches  138;  Conservative   53;  Mismatches  101;  Indels   31;  Gaps   12;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTC---LCGMAGNSMVIWLLGFRMH 57
              |: |:   ||  : :|    |       |    | : ||   | |: ||::|:|||| ||
Db          1 MDPTVPVLGTKLTPIN---GREETPCYKQTLSFTVLTCIISLVGLTGNAVVLWLLGCRMR 57

Qy         58 RNPFCIYILNLAAADLLFLFSMASTLSLETQP--LVNTTDKVHELMKRLMYFAYTVGLSL 115
              ||   |||||||||| |||     :  :   |  |:| :  : :::  :| | |  |||:
Db         58 RNAVSIYILNLAAADFLFL-----SFQIIRSPLRLINISHLIRKILVSVMTFPYFTGLSM 112

Qy        116 LTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR- 174
              |:||||:||||||:|||::| || |||| || ||| | || : |    ||  ||     |
Db        113 LSAISTERCLSVLWPIWYRCRRPTHLSAVVCVLLWGLSLLFSMLEWRFCD-FLFSGADSS 171

Qy        175 -CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLVFLI 232
               |    | :  | ::  |  |: :||| | | :   |    |: | |||:| :| :|||||:
Db        172 WCETSDFIPVAWLI-FLCVVLCVSSLVLLVRILCGS---RKMPLTRLYVTILLTVLVFLL 227

Qy        233 CSLPLSIYWFVLYWLSLPPE-----MQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRL 287
              | ||  |   ::| : |   |     : ::| ||     ||::|||||:||| ||| |  |
Db        228 CGLPFGILGALIYRMHLNLEVLYCHVYLVCMSL----SSLNSSANPIIYFFVGSFR-QRQ 282

Qy        288 PTRSLGTVLQQALREEPELEGGE 310
              ::|  |||:||:::||:: ||
Db        283 NRQNLKLVLQRALQDKPEVDKGE 305


RESULT 12
SNS3_HUMAN
ID   SNS3_HUMAN     STANDARD;      PRT;   322 AA.
AC   Q8TDD9;
DT   01-OCT-2004 (Rel. 45, Created)
DT   01-OCT-2004 (Rel. 45, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Sensory neuron-specific G-protein coupled receptor 3.
GN   Name=SNSR3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX   MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nn815;
RA   Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA   Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA   Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,
```

```
RA   Dray A., Walker P., Ahmad S.;
RT   "Proenkephalin A gene products activate a new family of sensory
RT   neuron-specific GPCRs.";
RL   Nat. Neurosci. 5:201-209(2002).
CC   -!- FUNCTION: Orphan receptor. Probably involved in the function of
CC       nociceptive neurons. May regulate nociceptor function and/or
CC       development, including the sensation or modulation of pain.
CC       Potently activated by enkephalins including BAM22 (bovine adrenal
CC       medulla peptide 22) and BAM (8-22). BAM22 is the most potent
CC       compound and evoked a large and dose-dependent release of
CC       intracellular calcium in stably transfected cells. G(alpha)q
CC       proteins are involved in the calcium-signaling pathway.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
CC       root and trigeminal sensory neurons.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC       Mas subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF474989; AAL86880.2; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN        1     31       Extracellular (Potential).
FT   TRANSMEM     32     52       1 (Potential).
FT   DOMAIN       53     67       Cytoplasmic (Potential).
FT   TRANSMEM     68     88       2 (Potential).
FT   DOMAIN       89     96       Extracellular (Potential).
FT   TRANSMEM     97    117       3 (Potential).
FT   DOMAIN      118    144       Cytoplasmic (Potential).
FT   TRANSMEM    145    165       4 (Potential).
FT   DOMAIN      166    177       Extracellular (Potential).
FT   TRANSMEM    178    198       5 (Potential).
FT   DOMAIN      199    221       Cytoplasmic (Potential).
FT   TRANSMEM    222    242       6 (Potential).
FT   DOMAIN      243    254       Extracellular (Potential).
FT   TRANSMEM    255    275       7 (Potential).
FT   DOMAIN      276    322       Cytoplasmic (Potential).
FT   CARBOHYD     16     16       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   322 AA;  36287 MW;  4C43E33E52DCBFF5 CRC64;

  Query Match             32.6%;  Score 542;  DB 1;  Length 322;
  Best Local Similarity   42.1%;  Pred. No. 5.2e-33;
  Matches  136;  Conservative   57;  Mismatches   98;  Indels   32;  Gaps   13;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTC---LCGMAGNSMVIWLLGFRMH 57
              |: |::   |::: |    |:     |    || : ||   | |: ||::|:|||| ||
Db          1 MDPTVS---TLDTELTPINGTEETLCYKQTLSLTVLTCIVSLVGLTGNAVVLWLLGCRMR 57

Qy         58 RNPFCIYILNLAAADLLFL-----FSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVG 112
              || | |||||||||| |||     :|: | :|:           : :::  :| |:|  |
Db         58 RNAFSIYILNLAAADFLFLSGRLIYSLLSFISI--------PHTISKILYPVMMFSYFAG 109

Qy        113 LSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNE 172
              || |:|:||:|||||:|||::|||| |||| || ||| | || : |    |  ||
Db        110 LSFLSAVSTERCLSVLWPIWYRCHRPTHLSAVVCVLLWALSLLRSILEWMLCG-FLFSGA 168

Qy        173 DR--CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLV 229
              |  |   | : | ::  |  |:  ||| | : :   |   |: | |||:| :| :|||
Db        169 DSAWCQTSDFITVAWLI-FLCVVLCGSSLVLLIRILCGS---RKIPLTRLYVTILLTVLV 224

Qy        230 FLICSLPLSIYWFVLYWLSLPPEMQVLC--FSLSRLSSSVSSSANPVIYFLVGSRRSHRL 287
              ||:| ||  | :|:  |: :  |: : |    :|   |:::|||||:||| ||| |  |
```

```
Db        225 FLLCGLPFGIQFFLFLWIHVDREV-LFCHVHLVSIFLSALNSSANPIIYFFVGSLR-QRQ 282

Qy        288 PTRSLGTVLQQALREEPEL-EGG 309
                ::|  |||:||:: ||: |||
Db        283 NRQNLKLVLQRALQDTPEVDEGG 305


RESULT 13
MRG1_HUMAN
ID   MRG1_HUMAN     STANDARD;      PRT;   322 AA.
AC   Q96LB2; Q8TDD8;
DT   01-OCT-2004 (Rel. 45, Created)
DT   01-OCT-2004 (Rel. 45, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Mas-related G-protein coupled receptor member X1 (Sensory neuron-
DE   specific G-protein coupled receptor 4).
GN   Name=MRGX1; Synonyms=SNSR4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21435808; PubMed=11551509;
RA   Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT   "A diverse family of GPCRs expressed in specific subsets of
RT   nociceptive sensory neurons.";
RL   Cell 106:619-632(2001).
RN   [2]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX   MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nn815;
RA   Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA   Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA   Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,
RA   Dray A., Walker P., Ahmad S.;
RT   "Proenkephalin A gene products activate a new family of sensory
RT   neuron-specific GPCRs.";
RL   Nat. Neurosci. 5:201-209(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22040266; PubMed=12044878;
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT   "Identification of G protein-coupled receptor genes from the human
RT   genome sequence.";
RL   FEBS Lett. 520:97-101(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Orphan receptor. Probably involved in the function of
CC       nociceptive neurons. May regulate nociceptor function and/or
CC       development, including the sensation or modulation of pain.
CC       Potently activated by enkephalins including BAM22 (bovine adrenal
CC       medulla peptide 22) and BAM (8-22). BAM22 is the most potent
CC       compound and evoked a large and dose-dependent release of
CC       intracellular calcium in stably transfected cells. G(alpha)q
CC       proteins are involved in the calcium-signaling pathway.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
CC       root and trigeminal sensory neurons.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC       Mas subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
```

```
CC   ----------------------------------------------------------------------
DR   EMBL; AY042213; AAK91804.1; -.
DR   EMBL; AF474990; AAL86881.1; -.
DR   EMBL; AB083628; BAB89341.1; -.
DR   EMBL; AB065846; BAC06064.1; -.
DR   MIM; 607227; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
FT   DOMAIN       1     31       Extracellular (Potential).
FT   TRANSMEM     32    52       1 (Potential).
FT   DOMAIN       53    67       Cytoplasmic (Potential).
FT   TRANSMEM     68    88       2 (Potential).
FT   DOMAIN       89    96       Extracellular (Potential).
FT   TRANSMEM     97    117      3 (Potential).
FT   DOMAIN       118   144      Cytoplasmic (Potential).
FT   TRANSMEM     145   165      4 (Potential).
FT   DOMAIN       166   177      Extracellular (Potential).
FT   TRANSMEM     178   198      5 (Potential).
FT   DOMAIN       199   221      Cytoplasmic (Potential).
FT   TRANSMEM     222   242      6 (Potential).
FT   DOMAIN       243   254      Extracellular (Potential).
FT   TRANSMEM     255   275      7 (Potential).
FT   DOMAIN       276   322      Cytoplasmic (Potential).
FT   CARBOHYD     16    16       N-linked (GlcNAc. . .) (Potential).
FT   VARIANT      36    36       I -> V (in dbSNP:11024885).
FT                               /FTId=VAR_019432.
FT   CONFLICT     5     5        I -> V (in Ref. 2).
SQ   SEQUENCE   322 AA;  36250 MW;  C7F3A9F4418E8AD1 CRC64;

  Query Match             32.4%;  Score 538.5;  DB 1;  Length 322;
  Best Local Similarity   41.3%;  Pred. No. 9.6e-33;
  Matches  135;  Conservative   59;  Mismatches  100;  Indels   33;  Gaps   13;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTC---LCGMAGNSMVIWLLGFRMH 57
              |: |::   |::: |    |:    |    || : ||   | |: ||::|:|||| ||
Db          1 MDPTIS---TLDTELTPINGTEETLCYKQTLSLTVLTCIVSLVGLTGNAVVLWLLGCRMR 57

Qy         58 RNPFCIYILNLAAADLLFL-----FSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVG 112
              || | |||||||||| |||     :|: | :|:          : :::  :| |:|  |
Db         58 RNAFSIYILNLAAADFLFLSGRLIYSLLSFISI--------PHTISKILYPVMMFSYFAG 109

Qy        113 LSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNE 172
              || |:|:||:|||||:|||::|||| |||| || ||| | || : |    |  ||
Db        110 LSFLSAVSTERCLSVLWPIWYRCHRPTHLSAVVCVLLWALSLLRSILEWMLCG-FLFSGA 168

Qy        173 DR--CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLV 229
              |    |   | :  | ::   |  |:  ||| | : :    |   |: | |||:| :| :|||
Db        169 DSAWCQTSDFITVAWLI-FLCVVLCGSSLVLLIRILCGS---RKIPLTRLYVTILLTVLV 224

Qy        230 FLICSLPLSIYWFVLYWLSLPPEMQVLC--FSLSRLSSSVSSSANPVIYFLVGSRRSHRL 287
              ||:| ||  | :|:  |: :  |: : |    :|   |:::|||||:||| ||| |  |
Db        225 FLLCGLPFGIQFFLFLWIHVDREV-LFCHVHLVSIFLSALNSSANPIIYFFVGSFR-QRQ 282

Qy        288 PTRSLGTVLQQALREEPELE--GGETP 312
              ::|  |||:||::  |::  ||: |
Db        283 NRQNLKLVLQRALQDASEVDEGGGQLP 309


RESULT 14
Q7TN42
ID   Q7TN42      PRELIMINARY;      PRT;   323 AA.
AC   Q7TN42;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   MRGC G protein-coupled receptor.
GN   Name=Mrgc;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=22810130; PubMed=12909716;
RA   Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;
RT   "Atypical expansion in mice of the sensory neuron-specific Mrg G
RT   protein-coupled receptor family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).
DR   EMBL; AF518245; AAQ08317.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   323 AA;  37136 MW;  50639FDAE42E8052 CRC64;

  Query Match             31.6%;  Score 525;  DB 2;  Length 323;
  Best Local Similarity   40.3%;  Pred. No. 1e-31;
  Matches  131;  Conservative   57;  Mismatches   95;  Indels   42;  Gaps   13;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTA---YLVLSSLAMFTCLCGMAGNSMVIWLLGFRMH 57
              |: |::|   |  : ||     | | :   | || |      | |:|||::|:|||||||
Db          1 MDPTISSLSTESTTLN----KTGHPSCRPILTLSFLVPIITLLGLAGNTIVLWLLGFRMR 56

Qy         58 RNPFCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKV--------HELMKRLM---- 105
              |    :|:|||: ||   ||                :::  ::         |:| | ::
Db         57 RKAISVYVLNLSLADSFFLCC----------HFIDSLMRIMNFYGIYAHKLSKEILGNVA 106

Qy        106 YFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCS 165
              :  |  |||:|:||||:||||||:|||: |||||::|| :| |:|  |  || |:    | |
Db        107 FIPYISGLSILSAISTERCLSVLWPIWYHCHRPRNMSAIICVLIWVLSFLM-GILDWFFS 165

Qy        166 KFLKFNEDRCFR-VDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVV 223
              ||        :: || :  | ::  |  ::  ||| | | :    |   ||:| :||:| :
Db        166 GFLGETHHHLWKNVDFIVTAFLI-FLFMLLFGSSLALLVRILCGS---RRKPLSRLYVTI 221

Qy        224 LASVLVFLICSLPLSIYWFVLYWLSLP---PEMQVLCFSLSRLSSSVSSSANPVIYFLVG 280
              :|:|:||| ||| :|  |:|||  :    |  :  : :: | | |:|||||:||||||
Db        222 SLTVMVYLICGLPLGLYLFLLYWFGIHLHYPFCHI--YQVTVLLSCVNSSANPIIYFLVG 279

Qy        281 SRRSHRLPTRSLGTVLQQALREEPE 305
              | | ||   |||  ||::|| | ||
Db        280 SFR-HRKKHRSLKMVLKRALEETPE 303


RESULT 15
MRG2_HUMAN
ID   MRG2_HUMAN     STANDARD;      PRT;   330 AA.
AC   Q96LB1;
DT   01-OCT-2004 (Rel. 45, Created)
DT   01-OCT-2004 (Rel. 45, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Mas-related G-protein coupled receptor member X2.
GN   Name=MRGX2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21435808; PubMed=11551509;
RA   Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT   "A diverse family of GPCRs expressed in specific subsets of
RT   nociceptive sensory neurons.";
RL   Cell 106:619-632(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
```

```
RX   MEDLINE=22040266; PubMed=12044878;
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT   "Identification of G protein-coupled receptor genes from the human
RT   genome sequence.";
RL   FEBS Lett. 520:97-101(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   TISSUE SPECIFICITY, AND POSSIBLE FUNCTION.
RX   PubMed=12915402; DOI=10.1074/jbc.M302456200;
RA   Robas N., Mead E., Fidock M.;
RT   "MrgX2 is a high potency cortistatin receptor expressed in dorsal root
RT   ganglion.";
RL   J. Biol. Chem. 278:44400-44404(2003).
CC   -!- FUNCTION: Orphan receptor. Probably involved in the function of
CC       nociceptive neurons. May regulate nociceptor function and/or
CC       development, including the sensation or modulation of pain.
CC       Cortistatin-14 seems to be a high potency ligand at this receptor.
CC       Cortistatin has several biological functions including roles in
CC       sleep regulation locomotor activity, and cortical function. In
CC       receptor-expressing cells, cortistatin-stimulated increases in
CC       intracellular Ca(2+) but had no effect on basal or forskolin-
CC       stimulated cAMP levels, suggesting that this receptor is G(q)-
CC       coupled.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Has a limited expression profile, both
CC       peripheral and within the central nervous system, with highest
CC       levels in dorsal root ganglion.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC       Mas subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY042214; AAK91805.1; -.
DR   EMBL; AB083626; BAB89339.1; -.
DR   EMBL; AB065811; BAC06030.1; -.
DR   EMBL; BC063450; AAH63450.1; -.
DR   MIM; 607228; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Polymorphism; Transmembrane.
FT   DOMAIN       1     33       Extracellular (Potential).
FT   TRANSMEM     34    54       1 (Potential).
FT   DOMAIN       55    63       Cytoplasmic (Potential).
FT   TRANSMEM     64    84       2 (Potential).
FT   DOMAIN       85    96       Extracellular (Potential).
FT   TRANSMEM     97    117      3 (Potential).
FT   DOMAIN       118   144      Cytoplasmic (Potential).
FT   TRANSMEM     145   165      4 (Potential).
FT   DOMAIN       166   184      Extracellular (Potential).
FT   TRANSMEM     185   205      5 (Potential).
FT   DOMAIN       206   228      Cytoplasmic (Potential).
FT   TRANSMEM     229   249      6 (Potential).
FT   DOMAIN       250   264      Extracellular (Potential).
FT   TRANSMEM     265   285      7 (Potential).
FT   DOMAIN       286   330      Cytoplasmic (Potential).
FT   VARIANT      62    62       N -> S (in dbSNP:10833049).
FT                               /FTId=VAR_019433.
SQ   SEQUENCE   330 AA;  37099 MW;  0B328FD78B1DF6BE CRC64;

  Query Match           31.4%;  Score 522;  DB 1;  Length 330;
  Best Local Similarity 39.1%;  Pred. No. 1.7e-31;
  Matches  133;  Conservative   58;  Mismatches  117;  Indels   32;  Gaps   12;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSS--------LAMFTCLCGMAGNSMVIWLL 52
              |: |  : ||  : :| :       | |:|          | :|  | |: ||  |:|||
Db          1 MDPTTPAWGTESTTVNGN-----DQALLLLCGKETLIPVFLILFIALVGLVGNGFVLWLL 55

Qy         53 GFRMHRNPFCIYILNLAAADLLFL-FSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTV 111
              |||| || | :|:|:|| || ||| | : : |   :    : :          :| ||
Db         56 GFRMRRNAFSVYVLSLAGADFLFLCFQIINCLVYLSNFFCSISINFPSFFTTVMTCAYLA 115

Qy        112 GLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFN 171
              |||:|: :||:|||||||:|||::| ||||||| || ||| | ||:: |   ||  ||  :
Db        116 GLSMLSTVSTERCLSVLWPIWYRCRRPRHLSAVVCVLLWALSLLLSILEGKFCG-FLFSD 174

Qy        172 EDR--CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVL 228
              |   |   | : || ::  |  |:  ||| | | :   |   |  | |||:: :| :||
Db        175 GDSGWCQTFDFITAAWLI-FLFMVLCGSSLALLVRILCGS---RGLPLTRLYLTILLTVL 230

Qy        229 VFLICSLPLSIYWFVLYWLSLPPEMQVLC--FSLSRLSSSVSSSANPVIYFLVGS-RRSH 285
              |||:| ||  | ||:: |:    :: : |    :| : ||::||||:||| ||| |:
Db        231 VFLLCGLPFGIQWFLILWIWKDSDV-LFCHIHPVSVVLSSLNSSANPIIYFFVGSFRKQW 289

Qy        286 RLPTRSLGTVLQQALREEPELEGGE------TPTVGTNEM 319
              ||   |  ||:||::  |::  |      || :  : :
Db        290 RLQQPILKLALQRALQDIAEVDHSEGCFRQGTPEMSRSSL 329


Search completed: November  4, 2004, 11:05:53
Job time : 194 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 4, 2004, 11:02:39 ; Search time 146 Seconds
(without alignments)
776.613 Million cell updates/sec

Title: US-09-801-944B-268
Perfect score: 1661
Sequence: 1 MNQTLNSSGTVESALNYSRG.....EEPELEGGETPTVGTNEMGA 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1661	100.0	321	9	US-09-920-068A-2	Sequence 2, Appli
2	1661	100.0	321	11	US-09-801-944B-268	Sequence 268, App
3	1661	100.0	321	14	US-10-188-405-2	Sequence 2, Appli
4	1661	100.0	321	14	US-10-183-116-35	Sequence 35, Appl
5	1661	100.0	321	14	US-10-079-384-8	Sequence 8, Appli
6	1661	100.0	321	14	US-10-017-161-1050	Sequence 1050, Ap
7	1661	100.0	321	14	US-10-258-768-1	Sequence 1, Appli
8	1661	100.0	321	14	US-10-239-421-2	Sequence 2, Appli
9	1661	100.0	321	14	US-10-305-555-4	Sequence 4, Appli
10	1661	100.0	321	14	US-10-088-726-19	Sequence 19, Appl
11	1661	100.0	321	14	US-10-321-807-10	Sequence 10, Appl
12	1661	100.0	321	14	US-10-237-467-8	Sequence 8, Appli
13	1661	100.0	321	14	US-10-182-822A-18	Sequence 18, Appl
14	1661	100.0	321	15	US-10-343-650A-42	Sequence 42, Appl
15	1661	100.0	321	16	US-10-321-807-10	Sequence 10, Appl
16	1661	100.0	321	16	US-10-314-048A-10	Sequence 10, Appl
17	1661	100.0	347	14	US-10-292-798-892	Sequence 892, App
18	1654	99.6	321	15	US-10-016-248-34	Sequence 34, Appl
19	1572	94.6	307	9	US-09-816-087-2	Sequence 2, Appli
20	1572	94.6	307	14	US-10-266-643-2	Sequence 2, Appli
21	1567	94.3	307	14	US-10-305-555-2	Sequence 2, Appli
22	921.5	55.5	321	15	US-10-016-248-80	Sequence 80, Appl
23	907	54.6	173	14	US-10-305-555-30	Sequence 30, Appl
24	892	53.7	170	14	US-10-305-555-26	Sequence 26, Appl
25	877	52.8	281	14	US-10-183-116-49	Sequence 49, Appl
26	553.5	33.3	322	14	US-10-292-798-1042	Sequence 1042, Ap
27	548.5	33.0	322	9	US-09-995-225-18	Sequence 18, Appl
28	548.5	33.0	322	10	US-09-995-225-18	Sequence 18, Appl
29	548.5	33.0	322	14	US-10-183-116-33	Sequence 33, Appl
30	548.5	33.0	322	14	US-10-225-567A-689	Sequence 689, App
31	548.5	33.0	322	14	US-10-237-467-4	Sequence 4, Appli
32	548.5	33.0	322	15	US-10-016-248-84	Sequence 84, Appl
33	548.5	33.0	322	15	US-10-072-012-531	Sequence 531, App
34	548.5	33.0	322	15	US-10-072-012-536	Sequence 536, App
35	538.5	32.4	322	14	US-10-183-116-16	Sequence 16, Appl
36	538.5	32.4	322	14	US-10-079-384-4	Sequence 4, Appli
37	538.5	32.4	322	14	US-10-017-161-1056	Sequence 1056, Ap
38	538.5	32.4	322	14	US-10-240-998-4	Sequence 4, Appli
39	538.5	32.4	322	14	US-10-321-807-20	Sequence 20, Appl
40	538.5	32.4	322	14	US-10-237-467-12	Sequence 12, Appl
41	538.5	32.4	322	14	US-10-292-798-898	Sequence 898, App
42	538.5	32.4	322	15	US-10-016-248-81	Sequence 81, Appl
43	538.5	32.4	322	15	US-10-072-012-172	Sequence 172, App
44	538.5	32.4	322	15	US-10-072-012-527	Sequence 527, App
45	538.5	32.4	322	15	US-10-072-012-533	Sequence 533, App

ALIGNMENTS

RESULT 1
US-09-920-068A-2
; Sequence 2, Application US/09920068A
; Patent No. US20020116724A1
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckhard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Polypeptides or Nucleic Acids Encoding
; TITLE OF INVENTION: These of a Family of G-Protein Coupled Receptors and their
; TITLE OF INVENTION: Use for the Diagnosis or Treatment of Disorders, for example
; TITLE OF INVENTION: Skin Disorders and their Use for the Identification of
; TITLE OF INVENTION: Pharmacologically Active Substances
; FILE REFERENCE: 50125/015002
; CURRENT APPLICATION NUMBER: US/09/920,068A
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/229,501
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: DE 10038111.1
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-068A-2

Query Match 100.0%; Score 1661; DB 9; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-145;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

```
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 2
US-09-801-944B-268
; Sequence 268, Application US/09801944B
; Publication No. US20040014169A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20040014169A1el G Protein-Coupled Receptors
; FILE REFERENCE: 00100US1
; CURRENT APPLICATION NUMBER: US/09/801,944B
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/187,828
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/187,715
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/187,929
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/187,930
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/187,825
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/187,833
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/187,830
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/187,829
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/187,582
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/187,581
; PRIOR FILING DATE: 2000-03-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 268
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-944B-268

Query Match 100.0%; Score 1661; DB 11; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-145;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 3
US-10-188-405-2
; Sequence 2, Application US/10188405
; Publication No. US20030082585A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Dai, Kang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Zhao, Jiagang
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030082585A1el Receptors
; FILE REFERENCE: 018781-008410US
; CURRENT APPLICATION NUMBER: US/10/188,405
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR2
US-10-188-405-2

Query Match 100.0%; Score 1661; DB 14; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-145;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

```
RESULT 4
US-10-183-116-35
; Sequence 35, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, David J.
;  APPLICANT:  Dong, Xinzhong
;  APPLICANT:  Zylka, Mark
;  APPLICANT:  Simon, Melvin
;  APPLICANT:  Han, Sang-kyou
;  TITLE OF INVENTION: PAIN SIGNALING MOLECULES
;  FILE REFERENCE: CALTE.4C1CP1
;  CURRENT APPLICATION NUMBER: US/10/183,116
;  CURRENT FILING DATE:  2002-06-26
;  PRIOR APPLICATION NUMBER: US 60/222,344
;  PRIOR FILING DATE: 2000-08-01
;  PRIOR APPLICATION NUMBER: US 60/202,027
;  PRIOR FILING DATE: 2000-05-04
;  PRIOR APPLICATION NUMBER: US 09/704,707
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: US 60/285,493
;  PRIOR FILING DATE: 2001-04-19
;  PRIOR APPLICATION NUMBER: US 09/849,869
;  PRIOR FILING DATE: 2001-05-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 321
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-183-116-35

  Query Match           100.0%;  Score 1661;  DB 14;  Length 321;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-145;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 5
US-10-079-384-8
; Sequence 8, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
;  APPLICANT: Communi, Didier
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: 9409/2132
;  CURRENT APPLICATION NUMBER: US/10/079,384
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: US 09/885,453
;  PRIOR FILING DATE: 2001-06-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 321
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-079-384-8

  Query Match           100.0%;  Score 1661;  DB 14;  Length 321;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-145;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 6
US-10-017-161-1050
; Sequence 1050, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
;  APPLICANT: SUWA, MAKIKO
;  APPLICANT:  ASAI, KIYOSHI
;  APPLICANT:  AKIYAMA, YUTAKA
;  APPLICANT:  ABURATANI, HIROYUKI
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 084335/0152
;  CURRENT APPLICATION NUMBER: US/10/017,161
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: JP 2001/246789
;  PRIOR FILING DATE: 2001-06-18
;  NUMBER OF SEQ ID NOS: 2430
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1050
;   LENGTH: 321
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-017-161-1050

  Query Match           100.0%;  Score 1661;  DB 14;  Length 321;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-145;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
```

```
Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 7
US-10-258-768-1
; Sequence 1, Application US/10258768
; Publication No. US20030153040A1
; GENERAL INFORMATION:
; APPLICANT: MORIIYA, Takeo
; APPLICANT: ITO, Takashi
; APPLICANT: SHINTANI, Yashushi
; APPLICANT: MATSUI, Hideki
; TITLE OF INVENTION: No. US20030153040A1el G Protein-Coupled Receptor and DNA Thereof
; FILE REFERENCE: 2721 US0P
; CURRENT APPLICATION NUMBER: US/10/258,768
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/JP01/03597
; PRIOR FILING DATE: 2001-4-26
; PRIOR APPLICATION NUMBER: JP 2000-130478
; PRIOR FILING DATE: 2000-4-28
; PRIOR APPLICATION NUMBER: JP 2000-140435
; PRIOR FILING DATE: 2000-5-12
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 1
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Human
US-10-258-768-1

Query Match 100.0%; Score 1661; DB 14; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-145;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 8
US-10-239-421-2
; Sequence 2, Application US/10239421
; Publication No. US20030153498A1
; GENERAL INFORMATION:
; APPLICANT: Shyman Ramakrishnan
; TITLE OF INVENTION: REGULATION OF HUMAN RTA-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 004974.00798
; CURRENT APPLICATION NUMBER: US/10/239,421
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/191,765
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-421-2

Query Match 100.0%; Score 1661; DB 14; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-145;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 9
US-10-305-555-4
; Sequence 4, Application US/10305555
; Publication No. US20030157525A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY31, AND VARIANTS AN
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: D0196 NP
; CURRENT APPLICATION NUMBER: US/10/305,555
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: U.S. 60/333,337
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: U.S. 60/355,619
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-305-555-4

Query Match 100.0%; Score 1661; DB 14; Length 321;

```
  Best Local Similarity   100.0%;  Pred. No. 1.3e-145;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 10
US-10-088-726-19
; Sequence 19, Application US/10088726
; Publication No. US20030157558A1
; GENERAL INFORMATION:
;  APPLICANT: Matsumoto et al.
;  TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS AN
;  TITLE OF INVENTION:  THEREOF, AND PRODUCTION AND USES THEREOF
;  FILE REFERENCE: 62514
;  CURRENT APPLICATION NUMBER: US/10/088,726
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: PCT/JP00/09408
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: JP   1999-375152
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: JP   2000-101339
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 321
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-088-726-19

  Query Match           100.0%;  Score 1661;  DB 14;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-145;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 11
US-10-321-807-10
; Sequence 10, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Rupong
;  APPLICANT:  Dang, Huong T.
;  APPLICANT:  Lowitz, Kevin P.
;  TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G P
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN0086
;  CURRENT APPLICATION NUMBER: US/10/321,807
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: US/09/714,008
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: PCT/US99/23938
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: 60/166,088
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/166,099
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/166,369
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/171,902
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/171,901
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/171,900
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/181,749
;  PRIOR FILING DATE: 2000-02-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 321
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-321-807-10

  Query Match           100.0%;  Score 1661;  DB 14;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-145;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

```
Db        241 WPVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 12
US-10-237-467-8
; Sequence 8, Application US/10237467
; Publication No. US20030186324A1
; GENERAL INFORMATION:
;  APPLICANT: Liao, Jiayu
;  APPLICANT:  Gray, Nathanael S.
;  APPLICANT:  Caldwell, Jeremy C.
;  APPLICANT:  Schultz, Peter G.
;  APPLICANT:  IRM LLC
;  TITLE OF INVENTION: Sensory Neuron Receptors
;  FILE REFERENCE: 021288-001300US
;  CURRENT APPLICATION NUMBER: US/10/237,467
;  CURRENT FILING DATE:  2003-01-14
;  PRIOR APPLICATION NUMBER: US 60/317,879
;  PRIOR FILING DATE: 2001-09-07
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 321
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR)
;   OTHER INFORMATION: 6 (DRG6) (X54KRCBYJQ4)
US-10-237-467-8

  Query Match             100.0%;  Score 1661;  DB 14;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-145;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WPVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WPVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 13
US-10-182-822A-18
; Sequence 18, Application US/10182822A
; Publication No. US20030211493A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.
;  APPLICANT:  AU-YOUNG, Janice; YUE, Henry
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: PI-0032 USN
;  CURRENT APPLICATION NUMBER: US/10/182,822A
;  CURRENT FILING DATE:  2001-02-01
;  PRIOR APPLICATION NUMBER: PCT/US 01/03455
;  PRIOR FILING DATE: 2001-01-02
;  PRIOR APPLICATION NUMBER: US 60/180,093
;  PRIOR FILING DATE: 2000-02-02
;  PRIOR APPLICATION NUMBER: US 60/182,045
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PERL Program
; SEQ ID NO 18
;   LENGTH: 321
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7472136CD1
US-10-182-822A-18

  Query Match             100.0%;  Score 1661;  DB 14;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-145;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WPVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WPVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 14
US-10-343-650A-42
; Sequence 42, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
;  APPLICANT: HAGA, TATSUYA
;  TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
;  FILE REFERENCE: 31671-186347
;  CURRENT APPLICATION NUMBER: US/10/343,650A
;  CURRENT FILING DATE:  2003-07-21
;  PRIOR APPLICATION NUMBER: JP 2000/237818
;  PRIOR FILING DATE: 2000-08-04
;  PRIOR APPLICATION NUMBER: JP 2001/34434
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 694
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 321
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-343-650A-42

  Query Match             100.0%;  Score 1661;  DB 15;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-145;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 15
US-10-321-807-10
; Sequence 10, Application US/10321807
; Publication No. US20040137563A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-10

Query Match 100.0%; Score 1661; DB 16; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-145;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

Search completed: November 4, 2004, 11:17:21
Job time : 148 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 4, 2004, 10:47:48 ; Search time 156 Seconds
(without alignments)
738.155 Million cell updates/sec

Title: US-09-801-944B-268
Perfect score: 1661
Sequence: 1 MNQTLNSSGTVESALNYSRG.....EEPELEGGETPTVGTNEMGA 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1661	100.0	321	4	AAU19292	Aau19292 Human G p
2	1661	100.0	321	4	AAG65582	Aag65582 Human RTA
3	1661	100.0	321	4	AAE06768	Aae06768 Human G-p
4	1661	100.0	321	4	AAG64124	Aag64124 Human G p
5	1661	100.0	321	4	AAU04366	Aau04366 Human G-p
6	1661	100.0	321	5	ABB04658	Abb04658 Human G p
7	1661	100.0	321	5	AAE17075	Aae17075 Human G-p
8	1661	100.0	321	5	ABB08770	Abb08770 Human G-p
9	1661	100.0	321	5	ABP95616	Abp95616 Human GPC
10	1661	100.0	321	6	ABP96694	Abp96694 Human G p
11	1661	100.0	321	6	ABP71374	Abp71374 Human TGR
12	1661	100.0	321	6	ABR62311	Abr62311 Human G-p
13	1661	100.0	321	7	ABW00805	Abw00805 Human GPC
14	1661	100.0	321	7	ADD29438	Add29438 Human G-p
15	1661	100.0	321	7	ADL96456	Adl96456 Human G p
16	1661	100.0	321	8	ADH08539	Adh08539 hMrgD. 3/
17	1661	100.0	321	8	ADO29546	Ado29546 Human GPC
18	1661	100.0	347	7	ADC86439	Adc86439 Human GPC
19	1657	99.8	321	7	ADC39134	Adc39134 Novel hum
20	1654	99.6	321	5	ABG79184	Abg79184 Human mas
21	1572	94.6	307	5	ABB79765	Abb79765 Human MAS
22	1572	94.6	307	6	ABU62646	Abu62646 Human MAS
23	1567	94.3	307	6	ABR62310	Abr62310 Human G-p
24	1480	89.1	409	5	AAE21298	Aae21298 Human Mrg
25	1399.5	84.3	308	7	ADC12708	Adc12708 Human GPC
26	921.5	55.5	320	3	AAY77734	Aay77734 Seven tim
27	921.5	55.5	321	8	ADO29547	Ado29547 Mouse GPC
28	912.5	54.9	319	3	AAY90513	Aay90513 Rat cereb
29	912.5	54.9	319	7	ADD29436	Add29436 Rat G-pro
30	877	52.8	281	5	AAE21305	Aae21305 Mouse Mrg
31	877	52.8	281	8	ADH08553	Adh08553 mMrgD. 3/
32	553.5	33.3	322	7	ADC86589	Adc86589 Human GPC
33	548.5	33.0	322	3	AAY87663	Aay87663 Human G p
34	548.5	33.0	322	5	ABJ04076	Abj04076 Human G p
35	548.5	33.0	322	5	AAE21297	Aae21297 Human Mrg
36	548.5	33.0	322	5	ADI17000	Adi17000 Human NOV
37	548.5	33.0	322	5	ADI16995	Adi16995 Human NOV
38	548.5	33.0	322	6	ABP96692	Abp96692 Human G p
39	548.5	33.0	322	6	ABP81758	Abp81758 Human Mrg
40	548.5	33.0	322	7	ADC17723	Adc17723 Human TGR
41	548.5	33.0	322	8	ADH08537	Adh08537 MrgX4. 3/
42	548.5	33.0	322	8	ADO29706	Ado29706 Human GPC
43	544.5	32.8	322	2	AAY30164	Aay30164 Human dor
44	544.5	32.8	322	3	AAY87664	Aay87664 Human G p
45	544.5	32.8	322	7	ADC17728	Adc17728 Human TGR

ALIGNMENTS

RESULT 1
AAU19292
ID AAU19292 standard; protein; 321 AA.
XX
AC AAU19292;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human G protein-coupled receptor nGPCR-74.
XX
KW Human; G protein-coupled receptor; nGPCR-x; antiviral; analgesic;
KW cytostatic; cardiant; antidiabetic; anoretic; hypotensive; hypertensive;
KW antiparkinsonian; nootropic; neuroprotective; antidepressant;
KW viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain;
KW cancer; metabolic disease; cardiovascular disease; type 2 diabetes;
KW obesity; anorexia; hypotension; hypertension; myocardial infarction;
KW atherosclerosis; Parkinson's disease; psychosis; neurological disorder;
KW schizophrenia; migraine; major depression; anxiety; mental disorder;
KW manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome.
XX
OS Homo sapiens.
XX
PN WO200166750-A2.
XX
PD 13-SEP-2001.
XX
PF 08-MAR-2001; 2001WO-US007322.
XX
PR 08-MAR-2000; 2000US-0187581P.
PR 08-MAR-2000; 2000US-0187582P.
PR 08-MAR-2000; 2000US-0187714P.
PR 08-MAR-2000; 2000US-0187715P.
PR 08-MAR-2000; 2000US-0187825P.
PR 08-MAR-2000; 2000US-0187828P.
PR 08-MAR-2000; 2000US-0187829P.
PR 08-MAR-2000; 2000US-0187830P.
PR 08-MAR-2000; 2000US-0187833P.
PR 08-MAR-2000; 2000US-0187874P.
PR 08-MAR-2000; 2000US-0187928P.
PR 08-MAR-2000; 2000US-0187929P.
PR 08-MAR-2000; 2000US-0187930P.
PR 08-MAR-2000; 2000US-0188049P.
PR 08-MAR-2000; 2000US-0189294P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Vogeli G, Wood LS;
XX

DR WPI; 2001-536778/59.
DR N-PSDB; AAS30861.
XX
PT Isolated nucleic acid molecules encoding G protein-coupled receptors
PT termed nGPCR-x, useful in the treatment and diagnosis of viral
PT infections, cancers and mental disorders (e.g. Parkinson's disease and
PT schizophrenia).
XX
PS Claim 31; Page 334-335; 336pp; English.
XX
CC The invention relates to novel isolated nucleic acid molecules encoding G
CC protein-coupled receptors termed nGPCR-x. nGPCR-x polynucleotides,
CC polypeptides, and modulators may be used in the treatment of diseases and
CC conditions such as infections, such as viral infections caused by HIV-1
CC (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and
CC cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity,
CC anorexia, hypotension, hypertension, myocardial infarction,
CC atherosclerosis), Parkinson's disease, and psychotic and neurological
CC disorders, including schizophrenia, migraine, major depression, anxiety,
CC mental disorder, manic depression, and dyskinesias, such as Huntington's
CC disease or Tourette's Syndrome and many other diseases and syndromes
CC listed in the specification. nGPCR-x polynucleotides and polypeptides, as
CC well as nGPCR-x modulators, may also be used in diagnostic assays for
CC such diseases or conditions. The present sequence represents a G protein-
CC coupled receptor of the invention
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 2
AAG65582
ID AAG65582 standard; protein; 321 AA.
XX
AC AAG65582;
XX
DT 07-JAN-2002 (first entry)
XX
DE Human RTA-like G protein-coupled receptor polypeptide.
XX
KW RTA-like G protein-coupled receptor; GPCR; antibacterial; virucide;
KW fungicide; protozoacide; cytostatic; antiasthmatic; antiparkinsonian;
KW hypotensive; antiallergic; antiulcer; analgesic; osteopathic; cardiant;
KW neuroprotective; nootropic; anticonvulsant; neuroleptic; hypertensive;
KW anorectic; human.
XX

OS Homo sapiens.
XX
PN WO200170814-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-EP003336.
XX
PR 24-MAR-2000; 2000US-0191765P.
XX
PA (FARB) BAYER AG.
XX
PI Ramakrishnan S;
XX
DR WPI; 2001-607525/69.
DR N-PSDB; AAH47755.
XX
PT Novel isolated polynucleotide encoding RTA-like-G protein-coupled
PT polypeptide useful for detecting diseases and abnormalities related to
PT presence of mutations in the polynucleotide.
XX
PS Claim 1; Fig 2; 76pp; English.
XX
CC This represents a human RTA-like G protein-coupled receptor (GPCR)
CC polypeptide. The RTA-like GPCR polypeptide can be expressed by standard
CC recombinant methodology. Pharmaceutical compositions comprising the
CC polypeptide or its modulators are useful for modulating the activity of
CC RTA-like GPCR in a disease such as bacterial, fungal, protozoan and viral
CC infection, pain, cancer, anorexia, bulimia, asthma, Parkinson's disease,
CC acute heart failure, hypotension, hypertension, urinary retention,
CC osteoporosis, angina pectoris, myocardial infarction, ulcer, allergy,
CC multiple sclerosis, benign prostatic hypertrophy, and psychotic and
CC neurological disorder, mental retardation and dyskinesia such as
CC Huntington's disease and Tourette's syndrome. The polypeptide is useful
CC to identify RTA analogs as well as a compound which may act as
CC somatostatin antagonists at the receptor sites, for raising specific
CC antibodies which can block the receptor, and as bait protein in a two-
CC hybrid or three-hybrid assay. Modulators of the polypeptide are useful in
CC treating various physiological disorders relating to abnormal control of
CC fluid and electrolyte homeostasis and in diseases associated with
CC abnormal angiotensin-induced aldosterone secretion, and in reversing
CC endogenous anorexia, in the control of bulimia, and in treating various
CC cardiovascular ailments such as caused by excessive pulmonary blood flow
CC or hypotension
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
```

```
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 3
AAE06768
ID   AAE06768 standard; protein; 321 AA.
XX
AC   AAE06768;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human G-protein coupled receptor-18 (GCREC-18) protein.
XX
KW   Human; G-protein coupled receptor-18; GCREC-18; cytostatic; hepatotropic;
KW   virucide; antiinflammatory; anticonvulsant; antiemetic; neuroprotective;
KW   nootropic; cerebroprotective; hypotensive; tranquilliser; vulnerary;
KW   ophthalmological; cell proliferative disorder; actinic keratosis;
KW   anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis;
KW   psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease;
KW   Huntington's disease; Parkinson's disease; cardiovascular disorder;
KW   epilepsy; hypertension; varicose vein; vasculitis; dysphagia; dyspepsia;
KW   anorexia; gastrointestinal disorder; pancreatitis; autoimmune disorder;
KW   Addison's disease; Crohn's disease; acquired immune deficiency syndrome;
KW   AIDS; uveitis; infection; trauma; metabolic disorder; diabetes; obesity;
KW   osteoporosis; transgenic animal; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          44. .78
FT                   /label= 7_transmembrane_receptor_domain
FT   Domain          104. .276
FT                   /label= 7_transmembrane_receptor_domain
FT   Domain          109. .129
FT                   /label= Transmembrane_domain
FT   Domain          229. .245
FT                   /label= Transmembrane_domain
XX
PN   WO200157085-A2.
XX
PD   09-AUG-2001.
XX
PF   01-FEB-2001; 2001WO-US003455.
XX
PR   02-FEB-2000; 2000US-0180093P.
PR   11-FEB-2000; 2000US-0182045P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Baughn MR,  Au-Young J,  Yue H;
XX
DR   WPI; 2001-488869/53.
DR   N-PSDB; AAD12961.
XX
PT   Novel isolated human G-protein coupled receptor useful for diagnosing,
PT   preventing and treating cell proliferative, neurological, cardiovascular,
PT   gastrointestinal, autoimmune/inflammatory and metabolic disorders.
XX
PS   Claim 1; Page 125; 138pp; English.
XX
CC   The present sequence is human G-protein coupled receptor-18 (GCREC-18)
CC   protein. The present invention relates to GCREC protein and nucleic acids
CC   encoding them. GCREC protein, its agonist or antagonist are useful for
CC   treating diseases or conditions associated with decreased expression or
CC   overexpression of functional GCREC in a patient, where the disorder is
CC   selected from cell proliferative disorders such as actinic keratosis,
CC   arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis, and
CC   cancer, neurological disorders such as epilepsy, stroke, Alzheimer's
CC   disease, Huntington's disease, Parkinson's disease, cardiovascular
CC   disorders such as hypertension, vasculitis, varicose veins, gastro-
CC   intestinal disorders such as dysphagia, dyspepsia, anorexia, nausea,
CC   pancreatitis, autoimmune/inflammatory disorders such as acquired
CC   immunodeficiency syndrome (AIDS), Addison's disease, Crohn's disease,
CC   uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic
CC   infections, trauma and metabolic disorders such as diabetes, obesity,
CC   osteoporosis. GCREC proteins and their cDNAs are used to assess the
CC   effects of exogenous compounds on the expression of GCREC sequences.
CC   GCREC cDNA is useful to create knock in humanised animals (pigs) or
CC   transgenic animals (mice or rats) to model human disease, for therapeutic
CC   or diagnostic purposes, for somatic or germline gene therapy, to generate
CC   hybridisation probes useful in mapping the naturally occurring genomic
CC   sequence, and in molecular biological techniques
XX
SQ   Sequence 321 AA;

  Query Match             100.0%;  Score 1661;  DB 4;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-181;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 4
AAG64124
ID   AAG64124 standard; protein; 321 AA.
XX
AC   AAG64124;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human G protein-coupled receptor GPRv51.
XX
KW   Human; guanosine triphosphate binding protein-coupled receptor;
KW   G protein-coupled receptor; GPRv8; GPRv12; GPRv16; GPRv21; GPRv40;
KW   GPRv47; GPRv51; GPRv71; GPRv72; cancer; liver cirrhosis;
KW   Alzheimer's disease; cytostatic; hepatotropic; nootropic;
KW   neuroprotective; gene therapy; peptide therapy.
XX
OS   Homo sapiens.
XX
PN   WO200148188-A1.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-JP009408.
XX
PR   28-DEC-1999;   99JP-00375152.
PR   31-MAR-2000; 2000JP-00101339.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Matsumoto S,  Oda T,  Saito Y,  Morikawa N,  Yoshida K,  Suwa M;
PI   Sugiyama T,  Kishimoto T,  Kanzaki K,  Yasuda S,  Inoue Y;
XX
```

DR WPI; 2001-425662/45.
DR N-PSDB; AAH73515.
XX
PT New DNA encoding guanosine triphosphate binding protein coupled receptors
PT and their expression products for screening potential anticancer and
PT nootropic drugs and in diagnosis of these diseases.
XX
PS Example 1; Page 130-132; 170pp; Japanese.
XX
CC The invention relates to nine human guanosine triphosphate binding
CC protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16,
CC GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPRv72, and to the genes
CC encoding them. These genes and proteins and antibodies against the
CC protein are useful in the treatment, prevention, diagnosis and
CC investigation of diseases associated with G protein-coupled receptors,
CC including cancer, cirrhosis of the liver and Alzheimer's disease. The
CC present sequence is a G protein-coupled receptor of the invention
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 5
AAU04366
ID AAU04366 standard; protein; 321 AA.
XX
AC AAU04366;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human G-protein coupled receptor, hRUP12.
XX
KW Human; G-protein coupled receptor; GPCR; hRUP12; agonist;
KW inverse agonist; lung cancer.
XX
OS Homo sapiens.
XX
PN WO200136471-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-US031509.
XX
PR 17-NOV-1999; 99US-0166088P.
PR 17-NOV-1999; 99US-0166099P.
PR 17-NOV-1999; 99US-0166369P.
PR 23-DEC-1999; 99US-0171900P.
PR 23-DEC-1999; 99US-0171901P.
PR 23-DEC-1999; 99US-0171902P.
PR 11-FEB-2000; 2000US-0181749P.
PR 14-MAR-2000; 2000US-0189258P.
PR 14-MAR-2000; 2000US-0189259P.
PR 10-APR-2000; 2000US-0195898P.
PR 10-APR-2000; 2000US-0195899P.
PR 10-APR-2000; 2000US-0196078P.
PR 28-APR-2000; 2000US-0200419P.
PR 12-MAY-2000; 2000US-0203630P.
PR 12-JUN-2000; 2000US-0210741P.
PR 12-JUN-2000; 2000US-0210982P.
PR 21-AUG-2000; 2000US-0226760P.
PR 26-SEP-2000; 2000US-0235418P.
PR 26-SEP-2000; 2000US-0235779P.
PR 20-OCT-2000; 2000US-0242332P.
PR 20-OCT-2000; 2000US-0242343P.
PR 24-OCT-2000; 2000US-0243019P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Lowitz KP;
XX
DR WPI; 2001-355616/37.
DR N-PSDB; AAS07939.
XX
PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents.
XX
PS Claim 17; Page 96-97; 160pp; English.
XX
CC The sequence represents a human G-protein coupled receptor (GPCR),
CC hRUP12. The endogenous and non-endogenous, constitutively activated
CC versions of human G-protein coupled receptors (GPCR), are useful for
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists having applicability as therapeutic
CC agents for treating diseases related to GPCR, e.g. lung cancer. Non-
CC endogenous version of human GPCRs are also utilized in research settings
CC and in vitro and in vivo system, incorporating GPCRs can be utilised to
CC elucidate and understand the roles these receptors play in the human
CC condition, both normal and diseased
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

```
RESULT 6
ABB04658
ID   ABB04658 standard; protein; 321 AA.
XX
AC   ABB04658;
XX
DT   04-MAR-2002  (first entry)
XX
DE   Human G protein-coupled receptor TGR7 SEQ ID NO:1.
XX
KW   Human; G protein-coupled receptor; TGR7; antiinflammatory; cytostatic;
KW   antidiabetic; neuroprotective; vulnerary; antiinfertility; inflammation;
KW   central nervous system disorder; CNS disorder; circulatory disorder;
KW   cancer; diabetes; infertility.
XX
OS   Homo sapiens.
XX
PN   WO200183748-A1.
XX
PD   08-NOV-2001.
XX
PF   26-APR-2001; 2001WO-JP003597.
XX
PR   28-APR-2000; 2000JP-00130478.
PR   12-MAY-2000; 2000JP-00140435.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Moriya T,  Ito T,  Shintani Y,  Matsui H;
XX
DR   WPI; 2002-082847/11.
DR   N-PSDB; ABA04371.
XX
PT   G-protein coupled receptor useful for treating CNS disorders,
PT   inflammation, circulatory disorders, cancer, diabetes and infertility.
XX
PS   Claim 1; Fig 2; 104pp; Japanese.
XX
CC   The present sequence represents a human G protein-coupled receptor
CC   designated TGR7. TGR7 has antiinflammatory, cytostatic, antidiabetic,
CC   neuroprotective, vulnerary and antiinfertility activities. TGR7 can be
CC   used in the treatment and prevention of central nervous system (CNS)
CC   disorders, inflammation, circulatory disorders, cancer, diabetes and
CC   infertility. TGR7 can also be used for producing antibodies and
CC   antiserums, for researching recombinant receptor expression structure,
CC   drug design, for producing probes and polymerase chain reaction (PCR)
CC   primers for genetic testing, and for producing transgenic animals
XX
SQ   Sequence 321 AA;

  Query Match             100.0%;  Score 1661;  DB 5;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-181;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321


RESULT 7
AAE17075
ID   AAE17075 standard; protein; 321 AA.
XX
AC   AAE17075;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human G-protein coupled receptor (GPCRx7) protein.
XX
KW   Human; G-protein coupled receptor; GPCRx7; cerebroprotective; vomiting;
KW   receptor-mediated disorder; therapy; urinary retention; allergy; obesity;
KW   osteoporosis; angina pectoris; restenosis; atherosclerosis; hypotension;
KW   anorexia; tumour; migraine; acute heart failure; ulcer; antiinflammatory;
KW   stroke; hypertension; neuronal disorder; myocardial infarction psychotic;
KW   depression; mental retardation; neurodegenerative disease; antibacterial;
KW   Alzheimer's disease; dementia; ischaemia; Parkinson's disease; antiviral;
KW   Huntington's disease; anxiety; antifungal; immunosuppressive; cytostatic;
KW   vulnerary; analgesic; anorectic; anabolic; diuretic; cardiant; nootropic;
KW   antiemetic; vasotropic; diabetes; cancer; tranquillizer; neuroleptic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          25. .54
FT                   /note= "Transmembrane domain"
FT   Domain          60. .80
FT                   /note= "Transmembrane domain"
FT   Domain          104. .132
FT                   /note= "Transmembrane domain"
FT   Domain          141. .164
FT                   /note= "Transmembrane domain"
FT   Domain          180. .205
FT                   /note= "Transmembrane domain"
FT   Domain          219. .243
FT                   /note= "Transmembrane domain"
FT   Domain          255. .278
FT                   /note= "Transmembrane domain"
XX
PN   WO200198330-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-BE000104.
XX
PR   20-JUN-2000; 2000US-0212913P.
PR   11-JUL-2000; 2000US-0217494P.
PR   26-JAN-2001; 2001EP-00870015.
PR   12-FEB-2001; 2001EP-00870024.
XX
PA   (EURO-) EUROSCREEN SA.
XX
PI   Lannoy V,  Brezillon S,  Detheux M,  Parmentier M,  Govarts C;
XX
DR   WPI; 2002-130789/17.
DR   N-PSDB; AAD27495.
XX
PT   New G-protein coupled receptor, useful in the manufacture of medicaments
PT   for treating receptor mediated disorders e.g. acute heart failure and
PT   Alzheimer's disease.
XX
PS   Disclosure; Page 25; 46pp; English.
XX
CC   The present invention relates to a G-protein coupled receptor (GPCR) and
CC   nucleotide encoding it. GPCR are useful in the manufacture of a
```

CC medicament for the prevention and/or treatment of receptor-mediated
CC disorders e.g. viral infections, virus and bacterial diseases, diseases
CC and disorders involving disturbances of cell migration, diseases or
CC perturbations of immune system including cancers, development of tumours
CC and tumour metastasis, inflammatory and neoplastic processes; bacterial
CC and fungal infections, in wound and bone healing, dysfunction of
CC regulatory growth functions; pains, diabetes, obesity, anorexia, bulimia,
CC urinary retention, osteoporosis, angina pectoris, atherosclerosis,
CC restenosis, diseases involving excessive or reduced proliferation or loss
CC of smooth muscle cells, aneurysm, stroke, ischaemia, ulcers, allergies,
CC benign prostatic hypertrophy, migraine, vomiting; blood circulating
CC affections including acute heart failure, hypotension, hypertension and
CC myocardial infarction psychotic; neuronal disorders such as anxiety,
CC schizophrenia, maniac depression, depression, delirium, dementia, severe
CC mental retardation; degenerative diseases; neurodegenerative diseases
CC such as Alzheimer's disease, Parkinson's disease; and dyskinesias e.g.
CC Huntington's disease or Gilles de la Tourette's syndrome and other
CC related diseases. The present sequence is GPCRx7 protein
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 5; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 8
ABB08770
ID ABB08770 standard; protein; 321 AA.
XX
AC ABB08770;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human G-protein coupled receptor SEQ ID NO 2.
XX
KW Mouse; human; G-protein coupled receptor; receptor; antipsoriatic;
KW antiulcer; dermatological; vulnerary; gene therapy; skin disease;
KW psoriasis; eczema; acne; wound healing; ulcer; transgenic.
XX
OS Homo sapiens.
XX
PN EP1178053-A2.
XX
PD 06-FEB-2002.
XX
PF 03-AUG-2001; 2001EP-00118709.
XX
PR 04-AUG-2000; 2000DE-01038111.
PR 31-AUG-2000; 2000US-0229501P.
XX
PA (SWIT-) SWITCH BIOTECH AG.
XX
PI Wolf E, Werner S, Halle J, Regenbogen J, Goppelt A;
XX
DR WPI; 2002-197547/26.
DR N-PSDB; ABL41225.
XX
PT New G protein coupled receptors, useful for diagnosis, treatment and
PT prevention of skin and wound-healing disorders, also related nucleic acid
PT and antibodies.
XX
PS Claim 1; Fig 5; 47pp; German.
XX
CC The invention relates to G-protein coupled receptor polypeptides (I,
CC ABB08769-ABB08772) or their functional variants with antipsoriatic,
CC antiulcer, dermatological and vulnerary activity. (I) and the nucleic
CC acids (II, ABL41224-ABL41227) encoding them, cells containing (II) and
CC antibodies specific for (I) are used for diagnosis, prevention or
CC treatment (including by gene therapy) of skin diseases, especially
CC psoriasis but also eczema, acne, urticaria and pigmentation disorders,
CC wounds and wound healing disorders, particularly ulcers and specifically
CC venous ulcers. The same materials (also transgenic animals containing
CC (II) in the genome) are used for identifying agents for treatment of
CC these disorders
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 5; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 9
ABP95616
ID ABP95616 standard; protein; 321 AA.
XX
AC ABP95616;
XX
DT 06-MAR-2003 (first entry)
XX
DE Human GPCR polypeptide SEQ ID NO 42.
XX
KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; receptor.
XX
OS Homo sapiens.
XX

PN WO200216548-A2.
XX
PD 28-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-IB001446.
XX
PR 04-AUG-2000; 2000JP-00237818.
PR 13-FEB-2001; 2001JP-00034434.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Haga T, Takeda S, Mitaku S;
XX
DR WPI; 2002-304118/34.
DR N-PSDB; ABZ42890.
XX
PT Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.
XX
PS Claim 10; SEQ ID NO 42; 97pp + Sequence Listing; Japanese.
XX
CC The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 5; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 10
ABP96694
ID ABP96694 standard; protein; 321 AA.
XX
AC ABP96694;
XX
DT 03-JUN-2003 (first entry)

XX
DE Human G protein-coupled receptor DRG6 protein SEQ ID NO:8.
XX
KW Human; G protein-coupled receptor; GPCR; DRG; pain; sensory transduction.
XX
OS Homo sapiens.
XX
PN WO2003023010-A2.
XX
PD 20-MAR-2003.
XX
PF 06-SEP-2002; 2002WO-US028619.
XX
PR 07-SEP-2001; 2001US-0317879P.
XX
PA (IRMI-) IRM LLC.
XX
PI Liao J, Gray NS, Caldwell JC, Schultz PG;
XX
DR WPI; 2003-301064/29.
DR N-PSDB; ACC44770.
XX
PT Novel G-protein coupled receptor polypeptide expressed in mammalian
PT sensory neurons of dorsal root ganglia, useful as target for screening
PT for agents that regulate pain.
XX
PS Claim 10; Page 50; 51pp; English.
XX
CC The present invention describes human G protein-coupled receptor (GPCR)
CC proteins (I) designated DRG1, DRG2, DRG4, DRG6, DRG7, and DRG8 (see
CC ABP96691 to ABP96696) encoded by ACC44767 to ACC44772. (I) can be used
CC for identifying a compound that modulates pain, by contacting a compound
CC with (I), and selecting a compound that binds to the extracellular domain
CC or that modulates GPCR activity of the polypeptide. Such compounds that
CC modulate the activity of (I) can be used to investigate the role of (I)
CC in sensory (e.g. pain) transduction. Biologically active (I) can be used
CC for testing inhibitors and activators of (I) as pain transducers or pain
CC inhibitors using in vivo and in vitro expression that measure e.g.
CC transcriptional activation of (I), ligand binding, phosphorylation and
CC dephosphorylation, binding to G-proteins, G-protein activation,
CC regulatory molecule binding, voltage, membrane potential and conductance
CC changes, ion flux, intracellular second messengers such as cAMP and
CC inositol triphosphate, intracellular calcium levels and neurotransmitter
CC release. Such activators and inhibitors identified using (I) can be used
CC to further study sensory transduction and to identify specific pain
CC agonists and antagonists. The modulators can be administered directly to
CC the mammalian subject for modulation of pain in vivo
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
```

```
Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 11
ABP71374
ID ABP71374 standard; protein; 321 AA.
XX
AC ABP71374;
XX
DT 28-APR-2003 (first entry)
XX
DE Human TGR2 protein.
XX
KW G-protein coupled receptor; GPCR; TGR2; TGR38; TGR118; TGR164; TGR343;
KW TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotropic;
KW anticonvulsant; hypotensive; hepatotropic; dermatological; human;
KW immunosuppressive; antiinflammatory.
XX
OS Homo sapiens.
XX
PN WO2003004678-A2.
XX
PD 16-JAN-2003.
XX
PF 01-JUL-2002; 2002WO-US020860.
XX
PR 03-JUL-2001; 2001US-0302800P.
XX
PA (TULA-) TULARIK INC.
XX
PI Tian H, Dai K, Chen J, Zhao J, Cutler G;
XX
DR WPI; 2003-210368/20.
DR N-PSDB; ABZ59167.
XX
PT New G-protein coupled receptor polypeptides designated TGR2, TGR38,
PT TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs
PT for treating or preventing e.g. asthma, multiple sclerosis, stroke or
PT nephrolithiasis.
XX
PS Claim 17; Page 58; 74pp; English.
XX
CC The invention provides new G-protein coupled receptor (GPCR) polypeptides
CC designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358 and encoding
CC polynucleotides. The polypeptides can be expressed by standard DNA
CC recombination methodology. The polypeptides are useful for screening or
CC identifying modulators of GPCR or signal transduction. The modulators of
CC signal transduction are useful for treating or preventing TGR-associated
CC disorders, e.g. asthma, multiple sclerosis or kidney disease. The
CC polypeptides are useful as targets for diagnosing or treating e.g.
CC epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia,
CC asymptomatic urinary abnormalities, hypertension, nephrolithiasis,
CC cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute
CC inflammatory dermatoses. The present sequence represents a human TGR2
CC protein
XX
SQ Sequence 321 AA;

```
  Query Match             100.0%;  Score 1661;  DB 6;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-181;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 12
ABR62311
ID ABR62311 standard; protein; 321 AA.
XX
AC ABR62311;
XX
DT 22-SEP-2003 (first entry)
XX
DE Human G-protein coupled receptor HGPRBMY31 splice variant.
XX
KW HGPRBMY31; human; G-protein coupled receptor; receptor; cytcstatic;
KW gynaecological; analgesic; antiparkinsonian; uropathic; nephrotrophic;
KW neuroprotective; nootropic; immunomodulator; gene therapy.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Domain   28. .49
FT   /note= "transmembrane domain"
FT Domain   61. .79
FT   /note= "transmembrane domain"
FT Domain   105. .127
FT   /note= "transmembrane domain"
FT Domain   141. .164
FT   /note= "transmembrane domain"
FT Domain   186. .205
FT   /note= "transmembrane domain"
FT Domain   219. .242
FT   /note= "transmembrane domain"
FT Domain   255. .278
FT   /note= "transmembrane domain"
XX
PN WO2003046147-A2.
XX
PD 05-JUN-2003.
XX
PF 26-NOV-2002; 2002WO-US038145.
XX
PR 26-NOV-2001; 2001US-0333337P.
PR 06-FEB-2002; 2002US-0355619P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Mintier GA, Ramanthan CS, Feder JN;
XX
DR WPI; 2003-505194/47.
DR N-PSDB; ACC83943.
XX
PT New nucleic acid encoding a human G-protein coupled receptor (GPCR) known
PT as HGPRBMY31 which is useful for screening or providing GPCR modulators
PT useful for treating diseases involving aberrant GPCR activity, e.g.
PT cancer.
XX
PS Claim 5; Fig 2; 219pp; English.
XX
CC This is the protein sequence of a splice variant of human HGPRBMY31, a

CC novel G-protein coupled receptor analogous to known G i/o coupled
CC receptors. HGPRBMY31 constitutively inhibits gene expression through the
CC cAMP response element (CRE). HGPRBMY31 (and its splice variant)
CC polynucleotides, polypeptides, agonists and antagonists are useful for
CC modulating intracellular cAMP levels, modulating cAMP sensitive
CC signalling pathways, and modulating CRE element associated signalling
CC pathways. They can also be used for genetic screening and for the
CC treatment of diseases, disorders, conditions or syndromes associated with
CC GPCRs, particularly: a reproductive disorder, such as a testicular
CC disorder or a cancer; a disorder related to aberrant G-protein coupled
CC signalling, particularly pathways that signal through the G alpha i/o
CC family of G-proteins; a disorder related to aberrant GPCR dependent cAMP
CC signalling or GPCR dependent signalling associated with CRE elements; an
CC immune disorder; a haematopoietic disorder; a disorder related to
CC aberrant T-cell maturation; leukaemia; multiple myeloma; related
CC proliferative condition of the immune or central nervous system; neural
CC disorder; brain cancer; hypersensitivity disorder; pain disorders; neural
CC disorder related to either a direct or indirect interaction with voltage-
CC gated sodium channels and their beta subunits; disorders related to
CC aberrations or injuries in the cerebellum, including cerebellar ataxias
CC of such as coeliac disease and other diseases associated with this region
CC of the brain, such as Rett syndrome, Parkinson's disease, von Hippel-
CC Lindau syndrome, familial congenital cerebellar hypoplasia and dysplastic
CC gangliocytoma of cerebellum; renal disorders; bladder disorders; urinary
CC incontinence; and overactive bladder (all claimed)
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 13
ABW00805
ID ABW00805 standard; protein; 321 AA.
XX
AC ABW00805;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human GPCRx7 protein.
XX
KW Human; G-protein coupled receptor; GPCR; infection; neoplastic process;
KW inflammation; myocardial infarction; atherosclerosis; angina pectoris;
KW hypertension; osteoporosis; antibacterial; cytostatic; fungicide; pain;
KW diabetes; cancer; virucide; analgesic; cardiant.
XX
OS Homo sapiens.
XX
PN US2003108986-A1.
XX
PD 12-JUN-2003.
XX
PF 20-FEB-2002; 2002US-00079384.
XX
PR 21-JUN-2001; 2001US-00885453.
XX
PA (EURO-) EUROSCREEN SA.
XX
PI Communi D, Lannoy V, Brezillon S, Detheux M, Parmentier M;
PI Govaerts C;
XX
DR WPI; 2003-810852/76.
DR N-PSDB; AAD61649.
XX
PT Novel G-protein coupled receptor useful for treating viral infections,
PT bacterial infections, fungal infections, cancer, diabetes, hypertension,
PT osteoporosis, angina pectoris, myocardial infarction, atherosclerosis.
XX
PS Claim 1; Fig 5; 0pp; English.
XX
CC The present invention relates to novel G-protein coupled receptors
CC (GPCRs) and the nucleic acids encoding them. The invention is useful for
CC treating viral, bacterial and fungal infections, inflammatory and
CC neoplastic processes, pain, diabetes, hypertension, osteoporosis, cancer,
CC angina pectoris, myocardial infarction and atherosclerosis. The present
CC sequence is human G-protein coupled receptor (GPCR) protein
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

RESULT 14
ADD29438
ID ADD29438 standard; protein; 321 AA.
XX
AC ADD29438;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human G-protein coupled receptor amino acid sequence.
XX
KW central nervous system; peripheral nervous system;
KW G protein coupled receptor; tranquiliser; neuroleptic; anticonvulsant;

KW uropathic; hypotensive; vasotropic; neuroprotective; vulnerary;
KW analgesic; hypnotic sedative; muscle relaxant; anaesthetic potentiator;
KW anxiety; cramp; schizophrenia; epilepsy; incontinence;
KW nervous hypertension; miscarriage; premature labour; male impotence;
KW cerebrovascular damage; infantile cerebral paralysis;
KW cramp type spinal paralysis; spinal vascular damage; multiple sclerosis;
KW spinocerebellar degeneration; external wounding; surgery; pain;
KW hyperaesthesia; numbness; human.
XX
OS Homo sapiens.
XX
PN WO2003082320-A1.
XX
PD 09-OCT-2003.
XX
PF 27-MAR-2003; 2003WO-JP003828.
XX
PR 28-MAR-2002; 2002JP-00093045.
PR 13-DEC-2002; 2002JP-00361580.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ito Y, Shinohara T, Hosoya M, Hinuma S, Noguchi Y;
XX
DR WPI; 2003-803966/75.
DR N-PSDB; ADD29437.
XX
PT Central or peripheral nervous system function modifier comprising G
PT protein coupled receptors for example for the treatment of anxiety,
PT cramp, schizophrenia, epilepsy, or incontinence.
XX
PS Claim 1; SEQ ID NO 4; 143pp; Japanese.
XX
CC This invention relates to a novel central or peripheral nervous system
CC function modifier which comprises a G protein coupled receptor. The
CC invention may have tranquiliser, neuroleptic, anticonvulsant, uropathic,
CC hypotensive, vasotropic, neuroprotective, vulnerary or analgesic
CC activities. The invention may be useful as a hypnotic sedative, muscle
CC relaxant, anaesthetic potentiator, for the treatment and prevention of
CC anxiety, cramp, schizophrenia, epilepsy, incontinence, nervous
CC hypertension, miscarriage, premature labour, male impotence,
CC cerebrovascular damage, infantile cerebral paralysis, cramp type spinal
CC paralysis, spinal vascular damage, multiple sclerosis, spinocerebellar
CC degeneration, after effects of external wounding, surgery, pain,
CC hyperaesthesia and numbness. The present sequence is the amino acid
CC sequence of a human G-protein coupled receptor of the invention.
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
```

Qy 301 REEPELEGGETPTVGTNEMGA 321
||||||||||||||||||||
Db 301 REEPELEGGETPTVGTNEMGA 321

RESULT 15
ADL96456
ID ADL96456 standard; protein; 321 AA.
XX
AC ADL96456;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human G protein-coupled receptor (GPCR) polypeptide #5.
XX
KW Human; G protein-coupled receptor; GPCR; receptor.
XX
OS Homo sapiens.
XX
PN US2003166148-A1.
XX
PD 04-SEP-2003.
XX
PF 16-DEC-2002; 2002US-00321807.
XX
PR 13-OCT-1998; 98US-00170496.
PR 16-NOV-2000; 2000US-00714008.
XX
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LOWI/) LOWITZ K P.
XX
PI Chen R, Dang HT, Lowitz KP;
XX
DR WPI; 2003-898073/82.
DR N-PSDB; ADL96455.
XX
PT New G protein-coupled receptor (GPCR), useful for preparing a composition
PT for identifying compounds as receptors, inverse agonists or partial
PT agonists having potential applicability as therapeutic agents.
XX
PS Claim 17; SEQ ID NO 10; 82pp; English.
XX
CC The invention relates to G protein-coupled receptor (GPCR) polypeptides
CC and the polynucleotides encoding them. The GPCR polypeptides are useful
CC for preparing a composition for identifying compounds as receptors,
CC inverse agonists or partial agonists, having potential applicability as
CC therapeutic agents. This sequence represents a human GPCR polypeptide of
CC the invention.
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1661; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.3e-181;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM 180

Qy        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIY 240

Qy        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQAL 300

Qy        301 REEPELEGGETPTVGTNEMGA 321
              |||||||||||||||||||||
Db        301 REEPELEGGETPTVGTNEMGA 321
```

Search completed: November 4, 2004, 11:01:52
Job time : 160 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 4, 2004, 10:56:44 ; Search time 39 Seconds
(without alignments)
545.848 Million cell updates/sec

Title: US-09-801-944B-268
Perfect score: 1661
Sequence: 1 MNQTLNSSGTVESALNYSRG.....EEPELEGGETPTVGTNEMGA 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	544.5	32.8	322	4	US-09-254-227A-13	Sequence 13, Appl
2	539.5	32.5	322	4	US-09-254-227A-11	Sequence 11, Appl
3	537.5	32.4	322	4	US-09-254-227A-9	Sequence 9, Appli
4	537	32.3	322	4	US-09-254-227A-7	Sequence 7, Appli
5	525	31.6	337	4	US-09-254-227A-1	Sequence 1, Appli
6	510	30.7	322	4	US-09-254-227A-3	Sequence 3, Appli
7	492	29.6	322	4	US-09-254-227A-5	Sequence 5, Appli
8	435.5	26.2	298	1	US-08-118-270-76	Sequence 76, Appl
9	435.5	26.2	298	5	PCT-US93-08528-76	Sequence 76, Appl
10	397.5	23.9	325	6	5320941-2	Patent No. 5320941
11	364.5	21.9	282	1	US-08-118-270-52	Sequence 52, Appl
12	364.5	21.9	282	5	PCT-US93-08528-52	Sequence 52, Appl
13	244	14.7	356	4	US-09-170-496D-246	Sequence 246, App
14	243	14.6	356	4	US-09-170-496D-270	Sequence 270, App
15	240.5	14.5	350	2	US-08-458-970A-9	Sequence 9, Appli
16	239	14.4	395	3	US-08-981-825-6	Sequence 6, Appli
17	239	14.4	395	3	US-09-480-784-6	Sequence 6, Appli
18	217.5	13.1	304	1	US-08-118-270-35	Sequence 35, Appl
19	217.5	13.1	304	5	PCT-US93-08528-35	Sequence 35, Appl
20	214.5	12.9	364	2	US-08-458-970A-10	Sequence 10, Appl
21	207.5	12.5	391	3	US-08-120-601B-8	Sequence 8, Appli
22	206.5	12.4	351	4	US-09-944-807-2	Sequence 2, Appli
23	202.5	12.2	391	1	US-07-816-283-2	Sequence 2, Appli
24	202.5	12.2	391	1	US-07-816-283-4	Sequence 4, Appli
25	202.5	12.2	391	1	US-08-417-103-2	Sequence 2, Appli
26	202.5	12.2	391	1	US-08-417-103-4	Sequence 4, Appli
27	202.5	12.2	391	1	US-08-417-103-14	Sequence 14, Appl
28	201.5	12.1	482	4	US-09-117-440-2	Sequence 2, Appli
29	200.5	12.1	482	2	US-08-876-874-2	Sequence 2, Appli
30	196	11.8	369	1	US-07-816-283-8	Sequence 8, Appli
31	196	11.8	369	1	US-08-417-103-8	Sequence 8, Appli
32	193.5	11.6	346	4	US-09-170-496D-254	Sequence 254, App
33	193.5	11.6	374	3	US-09-045-583-48	Sequence 48, Appl
34	193.5	11.6	374	4	US-09-534-185-48	Sequence 48, Appl
35	193.5	11.6	401	2	US-08-820-521-2	Sequence 2, Appli
36	193.5	11.6	401	3	US-09-248-715-2	Sequence 2, Appli
37	193.5	11.6	401	3	US-09-248-715-2	Sequence 2, Appli
38	193	11.6	355	4	US-09-170-496D-164	Sequence 164, App
39	193	11.6	369	2	US-08-411-859-3	Sequence 3, Appli
40	193	11.6	369	3	US-08-387-707-9	Sequence 9, Appli
41	193	11.6	369	4	US-08-405-271A-9	Sequence 9, Appli
42	192.5	11.6	346	4	US-09-170-496D-274	Sequence 274, App
43	192	11.6	355	4	US-09-170-496D-2	Sequence 2, Appli
44	192	11.6	389	3	US-08-430-286A-7	Sequence 7, Appli
45	191	11.5	365	4	US-09-503-219B-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-254-227A-13
; Sequence 13, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-13

Query Match 32.8%; Score 544.5; DB 4; Length 322;
Best Local Similarity 41.9%; Pred. No. 2.7e-41;
Matches 134; Conservative 56; Mismatches 105; Indels 25; Gaps 10;

```
Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60
              |: |:   ||  : :|    :  :   |  : |      | |: ||::|:||||:|| ||
Db          1 MDPTVPVFGTKLTPINGREETPCYNQTLSFTVLTCIISLVGLTGNAVVLWLLGYRMRRNA 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQP--LVNTTDKVHELMKRLMYFAYTVGLSLLTA 118
              ||||||||||| |||     :  :   |  |:| :  : :::  :| | |  |||:|:|
Db         61 VSIYILNLAAADFLFL-----SFQIIRSPLRLINISHLIRKILVSVMTFPYFTGLSMLSA 115

Qy        119 ISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR--CF 176
              |||:||||||:|||::|  || |||| || ||| | || : |   ||  ||     |   |
Db        116 ISTERCLSVLWPIWYRCRRPTHLSAVVCVLLWGLSLLFSMLEWRFCD-FLFSGADSSWCE 174

Qy        177 RVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLVFLICSL 235
                | :    ::  |  |: :||| | | :   |    |: | |||:| :| :|||||:| |
Db        175 TSDFIPVVWLI-FLCVVLCVSSLVLLVRILCGS---RKMPLTRLYVTILLTVLVFLLCGL 230

Qy        236 PLSIYWFVLYWLSLPPE-----MQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTR 290
              |  |   ::| : |  |     : ::| ||    ||::|||||:||| ||| |  |   :
Db        231 PFGILGALIYRMHLNLEVLYCHVYLVCMSL----SSLNSSANPIIYFFVGSFR-QRQNRQ 285

Qy        291 SLGTVLQQALREEPELEGGE 310
              :|  |||:||:::||:: ||
Db        286 NLKLVLQRALQDKPEVDKGE 305
```

```
RESULT 2
US-09-254-227A-11
; Sequence 11, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
;  APPLICANT:  Ahmad, Sultan
;  APPLICANT:  Banville, Denis
;  APPLICANT:  Fortin, Yves
;  APPLICANT:  Lembo, Paola
;  APPLICANT:  O'Donnell, Dajan
;  APPLICANT:  Shi-Hsiang, Shen
;  TITLE OF INVENTION:  G Protein-Coupled Receptors from the Rat and Human
;  FILE REFERENCE:  81823/268117
;  CURRENT APPLICATION NUMBER: US/09/254,227A
;  CURRENT FILING DATE:  1999-03-03
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 11
;  LENGTH: 322
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-254-227A-11

  Query Match            32.5%;  Score 539.5;  DB 4;  Length 322;
  Best Local Similarity  42.4%;  Pred. No. 7.5e-41;
  Matches  137;  Conservative   54;  Mismatches  101;  Indels   31;  Gaps   12;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTC---LCGMAGNSMVIWLLGFRMH 57
              |: |:   ||  : :|   |      |     | : ||   | |: ||::|:|||| ||
Db          1 MDPTVPVLGTKLTPIN---GREETPCYKQTLSFTVLTCIISLVGLTGNAVVLWLLGCRMR 57

Qy         58 RNPFCIYILNLAAADLLFLFSMASTLSLETQP--LVNTTDKVHELMKRLMYFAYTVGLSL 115
              ||   |||||||||| |||     :  :  :|  |:| :  : :::  :| | |  |||:
Db         58 RNAVSIYILNLAAADFLFL-----SFQIICRPLRLINISHLIRKILVSVMTFPYFTGLSM 112

Qy        116 LTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR- 174
              |:||||:||||||:|||::| || |||| || |||   || :  |   ||  ||   |
Db        113 LSAISTERCLSVLWPIWYRCRRPTHLSAVVCVLLWAGLLLFSMLEWRFCD-FLFSGADSS 171

Qy        175 -CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLVFLI 232
               |    | :  | ::  |  |: :||| | | :   |   |: | |||:| :| :|||||:
Db        172 WCETSDFIPVAWLI-FLCVVLCVSSLVLLVRILCGS---RKMPLTRLYVTILLTVLVFLL 227

Qy        233 CSLPLSIYWFVLYWLSLPPE-----MQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRL 287
              | ||  |   ::| : |  |      : ::| ||    ||::|||||:||| ||| |  |
Db        228 CGLPFGILGALIYRMHLNLEVLYCHVYLVCMSL----SSLNSSANPIIYFFVGSFR-QRQ 282

Qy        288 PTRSLGTVLQQALREEPELEGGE 310
              ::|  |||:||:::||:: ||
Db        283 NRQNLKLVLQRALQDKPEVDKGE 305


RESULT 3
US-09-254-227A-9
; Sequence 9, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
;  APPLICANT:  Ahmad, Sultan
;  APPLICANT:  Banville, Denis
;  APPLICANT:  Fortin, Yves
;  APPLICANT:  Lembo, Paola
;  APPLICANT:  O'Donnell, Dajan
;  APPLICANT:  Shi-Hsiang, Shen
;  TITLE OF INVENTION:  G Protein-Coupled Receptors from the Rat and Human
;  FILE REFERENCE:  81823/268117
;  CURRENT APPLICATION NUMBER: US/09/254,227A
;  CURRENT FILING DATE:  1999-03-03
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 9
;  LENGTH: 322
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-254-227A-9

  Query Match            32.4%;  Score 537.5;  DB 4;  Length 322;
  Best Local Similarity  41.3%;  Pred. No. 1.1e-40;
  Matches  135;  Conservative   59;  Mismatches  100;  Indels   33;  Gaps   13;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTC---LCGMAGNSMVIWLLGFRMH 57
              |: |::   |::: |    |:     |    || : ||   | |: ||::|:|||| ||
Db          1 MDPTVS---TLDTELTPINGTEETLCYKQTLSLTVLTCIVSLVGLTGNAVVLWLLGCRMR 57

Qy         58 RNPFCIYILNLAAADLLFL-----FSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVG 112
              || | |||||||||| |||     :|: | :|:          : :::  :| |:|  |
Db         58 RNAFSIYILNLAAADFLFLSGRLIYSLLSFISI--------PHTISKILYPVMMFSYFAG 109

Qy        113 LSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNE 172
              || |:|:||:||||||:|||::|||| |||| || ||| | || : |    |  ||
Db        110 LSFLSAVSTERCLSVLWPIWYRCHRPTHLSAVVCVLLWALSLLRSILEWMLCG-FLFSGA 168

Qy        173 DR--CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLV 229
              |   |   | :  | ::  |  |:  ||| | : :   |    |: | |||:| :| :|||
Db        169 DSAWCQTSDFITVAWLI-FLCVVLCGSSLVLLIRILCGS---RKIPLTRLYVTILLTVLV 224

Qy        230 FLICSLPLSIYWFVLYWLSLPPEMQVLC--FSLSRLSSSVSSSANPVIYFLVGSRRSHRL 287
              ||:| ||  | :|:  |: :  |: : |    :|   |:::|||||:||| ||| |  |
Db        225 FLLCGLPFGIQFFLFLWIHVDREV-LFCHVHLVSIFLSALNSSANPIIYFFVGSFR-QRQ 282

Qy        288 PTRSLGTVLQQALREEPELE--GGETP 312
              ::|  |||:||::  |::  ||: |
Db        283 NRQNLKLVLQRALQDASEVDEGGGQLP 309


RESULT 4
US-09-254-227A-7
; Sequence 7, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
;  APPLICANT:  Ahmad, Sultan
;  APPLICANT:  Banville, Denis
;  APPLICANT:  Fortin, Yves
;  APPLICANT:  Lembo, Paola
;  APPLICANT:  O'Donnell, Dajan
;  APPLICANT:  Shi-Hsiang, Shen
;  TITLE OF INVENTION:  G Protein-Coupled Receptors from the Rat and Human
;  FILE REFERENCE:  81823/268117
;  CURRENT APPLICATION NUMBER: US/09/254,227A
;  CURRENT FILING DATE:  1999-03-03
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 7
;  LENGTH: 322
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-254-227A-7

  Query Match            32.3%;  Score 537;  DB 4;  Length 322;
  Best Local Similarity  41.8%;  Pred. No. 1.3e-40;
  Matches  135;  Conservative   57;  Mismatches   99;  Indels   32;  Gaps   13;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTC---LCGMAGNSMVIWLLGFRMH 57
              |: |::   |::: |    |:     |    || : ||   | |: ||::|:|||| ||
Db          1 MDPTVS---TLDTELTPINGTEETLCYKQTLSLTVLTCIVSLVGLTGNAVVLWLLGCRMR 57

Qy         58 RNPFCIYILNLAAADLLFL-----FSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVG 112
              || | |||||||||| |||     :|: | :|:          : :::  :| |:|  |
Db         58 RNAFSIYILNLAAADFLFLSGRLIYSLLSFISI--------PHTISKILYPVMMFSYFAG 109

Qy        113 LSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNE 172
              |: |:|:|| ||||||:|||::|||| |||| || ||| | || : |    |  ||
Db        110 LNFLSAVSTDRCLSVLWPIWYRCHRPTHLSAVVCVLLWALSLLRSILEWMLCG-FLFSGA 168

Qy        173 DR--CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLV 229
```

```
Db        169 DSAWCQTSDFITVAWLI-FLCVVLCGSSLVLLIRILCGS---RKIPLTRLYVTILLTVLV 224

Qy        230 FLICSLPLSIYWFVLYWLSLPPEMQVLC--FSLSRLSSSVSSSANPVIYFLVGSRRSHRL 287

Db        225 FLLCGLPFGIQFFLFLWIHVDREV-LFCHVHLVSIFLSALNSSANPIIYFFVGSLR-QRQ 282

Qy        288 PTRSLGTVLQQALREEPEL-EGG 309

Db        283 NRQNLKLVLQRALQDTPEVDEGG 305


RESULT 5
US-09-254-227A-1
; Sequence 1, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
;  APPLICANT:  Ahmad, Sultan
;  APPLICANT:  Banville, Denis
;  APPLICANT:  Fortin, Yves
;  APPLICANT:  Lembo, Paola
;  APPLICANT:  O'Donnell, Dajan
;  APPLICANT:  Shi-Hsiang, Shen
;  TITLE OF INVENTION:  G Protein-Coupled Receptors from the Rat and Human
;  FILE REFERENCE:  81823/268117
;  CURRENT APPLICATION NUMBER: US/09/254,227A
;  CURRENT FILING DATE:  1999-03-03
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 1
;  LENGTH: 337
;  TYPE: PRT
;  ORGANISM: rat
US-09-254-227A-1

  Query Match           31.6%;  Score 525;  DB 4;  Length 337;
  Best Local Similarity  40.3%;  Pred. No. 1.6e-39;
  Matches  131;  Conservative   57;  Mismatches   95;  Indels   42;  Gaps   13;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTA---YLVLSSLAMFTCLCGMAGNSMVIWLLGFRMH 57

Db         15 MDPTISSLSTESTTLN----KTGHPSCRPILTLSFLVPIITLLGLAGNTIVLWLLGFRMR 70

Qy         58 RNPFCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKV--------HELMKRLM---- 105

Db         71 RKAISVYVLNLSLADSFFLCC----------HFIDSLMRIMNFYGIYAHKLSKEILGNVA 120

Qy        106 YFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCS 165

Db        121 FIPYISGLSILSAISTERCLSVLWPIWYHCHRPRNMSAIICVLIWVLSFLM-GILDWFFS 179

Qy        166 KFLKFNEDRCFR-VDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVV 223

Db        180 GFLGETHHHLWKNVDFIVTAFLI-FLFMLLFGSSLALLVRILCGS---RRKPLSRLYVTI 235

Qy        224 LASVLVFLICSLPLSIYWFVLYWLSLP---PEMQVLCFSLSRLSSSVSSSANPVIYFLVG 280

Db        236 SLTVMVYLICGLPLGLYLFLLYWFGIHLHYPFCHI--YQVTVLLSCVNSSANPIIYFLVG 293

Qy        281 SRRSHRLPTRSLGTVLQQALREEPE 305

Db        294 SFR-HRKKHRSLKMVLKRALEETPE 317


RESULT 6
US-09-254-227A-3
; Sequence 3, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
;  APPLICANT:  Ahmad, Sultan
;  APPLICANT:  Banville, Denis
;  APPLICANT:  Fortin, Yves
;  APPLICANT:  Lembo, Paola
;  APPLICANT:  O'Donnell, Dajan
;  APPLICANT:  Shi-Hsiang, Shen
;  TITLE OF INVENTION:  G Protein-Coupled Receptors from the Rat and Human
;  FILE REFERENCE:  81823/268117
;  CURRENT APPLICATION NUMBER: US/09/254,227A
;  CURRENT FILING DATE:  1999-03-03
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 3
;  LENGTH: 322
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-254-227A-3

  Query Match           30.7%;  Score 510;  DB 4;  Length 322;
  Best Local Similarity  40.3%;  Pred. No. 3.4e-38;
  Matches  127;  Conservative   57;  Mismatches  115;  Indels   16;  Gaps    9;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Db          1 MDPTIPVLGTKLTPINGREETPCYNQTLSFTGLTCIISLVALTGNAVVLWLLGCRMRRNA 60

Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120

Db         61 VSIYILNLVAANFLFL---SGHIIFSPLPLINIRHPISKILSPVMTFPYFIGLSMLSAIS 117

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCS-KFLKFNEDRCFRVD 179

Db        118 TERCLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGANSVWCETSD 177

Qy        180 MVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLVFLICSLPLS 238

Db        178 FITIAWLV-FLCVVLCGSSLVLLVRILCGS---RKMPLTRLYVTILLTVLVFLLCGLPFG 233

Qy        239 IYWFVLYWLSLPPEMQVLCFSLSRLS---SSVSSSANPVIYFLVGSRRSHRLPTRSLGTV 295

Db        234 IQWALFSRIHL--DWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFR-QRQNRQNLKLV 290

Qy        296 LQQALREEPEL-EGG 309

Db        291 LQRALQDTPEVDEGG 305


RESULT 7
US-09-254-227A-5
; Sequence 5, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
;  APPLICANT:  Ahmad, Sultan
;  APPLICANT:  Banville, Denis
;  APPLICANT:  Fortin, Yves
;  APPLICANT:  Lembo, Paola
;  APPLICANT:  O'Donnell, Dajan
;  APPLICANT:  Shi-Hsiang, Shen
;  TITLE OF INVENTION:  G Protein-Coupled Receptors from the Rat and Human
;  FILE REFERENCE:  81823/268117
;  CURRENT APPLICATION NUMBER: US/09/254,227A
;  CURRENT FILING DATE:  1999-03-03
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 5
;  LENGTH: 322
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-254-227A-5

  Query Match           29.6%;  Score 492;  DB 4;  Length 322;
  Best Local Similarity  40.1%;  Pred. No. 1.4e-36;
  Matches  127;  Conservative   57;  Mismatches  113;  Indels   20;  Gaps   11;

Qy          1 MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNP 60

Db          1 MDPTVPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA 60
```

```
Qy         61 FCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
Db         61 VSIYILNLVAADFLFL---SGHIICSPLRLINISHPISKILSPVMTFPYFIGLSMLNAIS 117

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNED--RCFRV 178
Db        118 TERCLSILWPIWYHCRRPRYLSSVMCVLLWAPSLLRSILEWMFCD-FLFSGADSVRCETS 176

Qy        179 DMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQP-TRLFVVVLASVLVFLICSLPL 237
Db        177 DFITIAWLV-FLRVVLCGSSLVLLVRILCGS---RKMPLTRLYVTILLTVLVFLLCGLPF 232

Qy        238 SIYWFVLYWLSLPPEMQVLCFSLSRLS---SSVSSSANPVIYFLVGSRRSHRLPTR-SLG 293
Db        233 GIQWALFSRIHL--DWKVLFCHVHLVSIFLSALNSSANPIIYFFMGSFR--QLQNRKTLK 288

Qy        294 TVLQQALREEPEL-EGG 309
Db        289 LVLQRDLQDTPEVDEGG 305
```

RESULT 8
US-08-118-270-76
; Sequence 76, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-76

Query Match 26.2%; Score 435.5; DB 1; Length 298;
Best Local Similarity 35.2%; Pred. No. 1.6e-31;
Matches 106; Conservative 56; Mismatches 118; Indels 21; Gaps 8;

```
Qy         29 VLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIYI--LNLAAADLLFLFSMASTLSLE 86
Db          1 VTNYIFLLLCLCGLVGNGLVLWFFGFSIKRTPFSIYIYFLHIASADGIYLFSKAVIALLN 60

Qy         87 TQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVC 146
Db         61 MGTFLGSFPDYVRRVSRIVGLTFFAGVSLLPAISIERCVSVIFPMWYWRRRPKRLSAGVC 120

Qy        147 GLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM-VQAALIMGVLTPVMTLSSLTLFVWV 205
Db        121 ALLWLLSFLVTSIHNYFCLLGHEASGTACLNMDISLLGILLFFLFCPIMVLPCIALLHVE 180

Qy        206 RRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVLYWL-----SLPPEMQVLCFSL 260
Db        181 CRARR--RQRSAKLNHVVLAIVSVFLVSSIYLGIDWF-LFWVFQIPAPFPEYVRDLCI-- 235

Qy        261 SRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALRE--EPELEGGETPTVGTNE 318
Db        236 -----CINSSAKPIVYFIAGRDKSQRL-WEPLRVVFQRALRDGAEPGDAASSTPNTVTME 289

Qy        319 M 319
Db        290 M 290
```

RESULT 9
PCT-US93-08528-76
; Sequence 76, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-08528-76

Query Match 26.2%; Score 435.5; DB 5; Length 298;
Best Local Similarity 35.2%; Pred. No. 1.6e-31;
Matches 106; Conservative 56; Mismatches 118; Indels 21; Gaps 8;

```
Qy         29 VLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIYI--LNLAAADLLFLFSMASTLSLE 86
Db          1 VTNYIFLLLCLCGLVGNGLVLWFFGFSIKRTPFSIYIYFLHIASADGIYLFSKAVIALLN 60
```

```
Qy          87 TQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVC 146
Db          61 MGTFLGSFPDYVRRVSRIVGLTFFAGVSLLPAISIERCVSVIFPMWYWRRRPKRLSAGVC 120

Qy         147 GLLWTLCLLMNGLTSSFCSKFLKFNEDRCFRVDM-VQAALIMGVLTPVMTLSSLTLFVWV 205
Db         121 ALLWLLSFLVTSIHNYFCLLGHEASGTACLNMDISLLGILLFFLFCPIMVLPCIALLHVE 180

Qy         206 RRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVLYWL-----SLPPEMQVLCFSL 260
Db         181 CRARR--RQRSAKLNHVVLAIVSVFLVSSIYLGIDWF-LFWVFQIPAPFPEYVRDLCI-- 235

Qy         261 SRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALRE--EPELEGGETPTVGTNE 318
Db         236 -----CINSSAKPIVYFIAGRDKSQRL-WEPLRVVFQRALRDGAEPGDAASSTPNTVTME 289

Qy         319 M 319
               |
Db         290 M 290
```

RESULT 10
5320941-2
;Patent No. 5320941
; APPLICANT: Young, Dallan;Wigler, Michael H.;Fasano
;Ottavio
; TITLE OF INVENTION: DNA SEQUENCES ENCODING MAS ONHCOGENE,
;POLYPETIDES ENCODED THEREFROM AND DIAGNOSTIC AND OTHER METHODS
;BASED THEREFROM
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/06/872,087
; FILING DATE: 06-JUN-1986
;SEQ ID NO:2:
; LENGTH: 325
5320941-2

Query Match 23.9%; Score 397.5; DB 6; Length 325;
Best Local Similarity 31.8%; Pred. No. 4.9e-28;
Matches 101; Conservative 61; Mismatches 117; Indels 39; Gaps 9;

```
Qy           7 SSGTVESALNYSRG-----STVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPF 61
Db           7 TSFVVEEPTNISTGRNASVGNAHRQIPIVHWVIMSISPVGFVENGILLWFLCFRMRRNPF 66

Qy          62 CIYILNLAAADL-----LFLFSMASTLSLE-------TQPLVNTTDKVHELMKRLMYFAY 109
Db          67 TVYITHLSIADISLLFCIFILSIDYALDYELSSGHYYTIVTLSVT----------FLFGY 116

Qy         110 TVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFC--SKF 167
Db         117 NTGLYLLTAISVERCLSVLYPIWYRCHRPKYQSALVCALLWALSCLVTTMEYVMCIHTEE 176

Qy         168 LKFNEDRCFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASV 227
Db         177 ESDSPNDCPAVIIFIAILSFLVFTGLMLVSSTILVVKIPKNT--WASHSSKLYIVIMVTI 234

Qy         228 LVFLICSLPLSIYWFVL--YWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSH 285
Db         235 IIFLIFAMRMRLLYLLYYEYWSTFGN-----LHDISLLFSTINSSANNFIYFFVGSSKKK 289

Qy         286 RLPTRSLGTVLQQALREE 303
               |  :||  |  :| ::|
Db         290 RF-KQSLKVVTTRAFKDE 306
```

RESULT 11
US-08-118-270-52
; Sequence 52, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-52

Query Match 21.9%; Score 364.5; DB 1; Length 282;
Best Local Similarity 32.4%; Pred. No. 3.9e-25;
Matches 97; Conservative 57; Mismatches 90; Indels 55; Gaps 13;

```
Qy          23 VHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIYI-LNLAAADLLF-LFSMA 80
Db           2 VHWVIMSISPV-------GFVENGILLWFLCF------FTVYTHLSIADISLLFCIFILS 48

Qy          81 STLSLETQPLVNTTDKVHELMKRLMY----------FAYTVGLSLLTAISTQRCLSVLFP 130
Db          49 IDYALD-----------YELSSGHYYTIVTLSVTFLFGYNTGLYLLTAISVERCLSVLYP 97

Qy         131 IWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR----CFRVDMVQAALI 186
Db          98 IWYRCHRPKYQSALVCALLWALSCL---VTTMYVMCIDRFEESHSRNDCRAVIIFIAILS 154

Qy         187 MGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVL-- 244
Db         155 FLVFTP--SVSSTILVVKIRKNT--WASHSSKLYIVIMVTIIIFLIFAMPMRLLYLLYYE 210

Qy         245 YWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREE 303
Db         211 YWSTFGN-----LHHISLLFSTINSSANPFIYFFVGSSKKKRF-KESLKVVLTRAFKDE 263
```

RESULT 12
PCT-US93-08528-52
; Sequence 52, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:

```
;       ADDRESSEE:  BROWDY AND NEIMARK
;       STREET:  419 Seventh Street, N.W., Suite 300
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/08528
;       FILING DATE:  09-SEP-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/943,236
;       FILING DATE:  10-SEP-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Townsend, Kevin G.
;       REGISTRATION NUMBER:  34,033
;       REFERENCE/DOCKET NUMBER:  MURPHY=2 PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;       TELEX:  248633
;   INFORMATION FOR SEQ ID NO:  52:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  282 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
PCT-US93-08528-52

  Query Match             21.9%;  Score 364.5;  DB 5;  Length 282;
  Best Local Similarity   32.4%;  Pred. No. 3.9e-25;
  Matches   97;  Conservative   57;  Mismatches   90;  Indels   55;  Gaps   13;

Qy         23 VHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIYI-LNLAAADLLF-LFSMA 80
              ||   : :| :       |   | :::| | |       | :|  |::|   ||| :| ::
Db          2 VHWVIMSISPV-------GFVENGILLWFLCF------FTVYTHLSIADISLLFCIFILS 48

Qy         81 STLSLETQPLVNTTDKVHELMKRLMY----------FAYTVGLSLLTAISTQRCLSVLFP 130
                :|:           :||     |          | |  || |||||| :||||||:|
Db         49 IDYALD-----------YELSSGHYYTIVTLSVTFLFGYNTGLYLLTAISVERCLSVLYP 97

Qy        131 IWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR----CFRVDMVQAALI 186
              ||::||||:: || || ||| | |   :|: :     :| |       |  | :  | |
Db         98 IWYRCHRPKYQSALVCALLWALSCL---VTTMYVMCIDRFEESHSRNDCRAVIIFIAILS 154

Qy        187 MGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVL-- 244
                | ||  ::||  | | :|:::   |    ::|::|:: ::::||| ::|: : : :
Db        155 FLVFTP--SVSSTILVVKIRKNT--WASHSSKLYIVIMVTIIIFLIFAMPMRLLYLLYYE 210

Qy        245 YWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREE 303
              || :             :| | |:::||||| ||| ||| :   |     ||  || :| ::|
Db        211 YWSTFGN-----LHHISLLFSTINSSANPFIYFFVGSSKKKRF-KESLKVVLTRAFKDE 263


RESULT 13
US-09-170-496D-246
; Sequence 246, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 246
;   LENGTH: 356
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-246

  Query Match             14.7%;  Score 244;  DB 4;  Length 356;
  Best Local Similarity   24.4%;  Pred. No. 3.8e-14;
  Matches   86;  Conservative   62;  Mismatches  139;  Indels   66;  Gaps   13;

Qy          2 NQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPF 61
              :: :|||| :   :   |  ||    ::||:    : : |: || :|:|:  ||| |
Db         26 SRKMNSSGCLSEEVGSLRPLTV----VILSA----SIVVGVLGNGLVLWMTVFRMARTVS 77

Qy         62 CIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRL----MYFAYTVGLSLLT 117
               :   :|| ||    | :: :| :    :|:    : |   :|    :: :|     ||
Db         78 TVCFFHLALAD----FMLSLSLPIAMYYIVSRQWLLGEWACKLYITFVFLSYFASNCLLV 133

Qy        118 AISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR--- 174
              ||  ||:|||:|:|   ||    ::|:   :|        | :: ||  |||   |
Db        134 FISVDRCISVLYPVWALNHRTVQRASWLAFGVWL-------LAAALCSAHLKFRTTRKWN 186

Qy        175 -------CFRVDMVQAAL----------------IMGVLTPVMTLSSLTLFVWVRRSSQ 210
                    |  |  | :                ::| | |:  : :   :  :
Db        187 GCTHCYLAFNSDNETAQIWIEGVVEGHIIGTIGHFLLGFLGPLAIIGTCAHLIRAKLLRE 246

Qy        211 QW--RRQPTRLFVVVLASVLVFLICSLPLSIYWFVLYWLSL------PPEMQVLCFSLSR 262
              |    :| || :|:::  :|     | ::   |  |  :       | | :|    |
Db        247 GWVHANRPARLLLVLVSAFFIFW---SPFNVVLLVHLWRRVMLKEIYHPRM-LLILQASF 302

Qy        263 LSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREEPELEG---GETP 312
                |:|| || :|  ||      :   :|| : | :|  ||  |     |  |
Db        303 ALGCVNSSLNPFLYVFVGRDFQEKF-FQSLTSALARAFGEEEFLSSCPRGNAP 354


RESULT 14
US-09-170-496D-270
; Sequence 270, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-C
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 270
;   LENGTH: 356
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-270

  Query Match             14.6%;  Score 243;  DB 4;  Length 356;
  Best Local Similarity   24.4%;  Pred. No. 4.7e-14;
  Matches   86;  Conservative   62;  Mismatches  139;  Indels   66;  Gaps   13;

Qy          2 NQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPF 61
              :: :|||| :   :   |  ||    ::||:    : : |: || :|:|:  ||| |
Db         26 SRKMNSSGCLSEEVGSLRPLTV----VILSA----SIVVGVLGNGLVLWMTVFRMARTVS 77

Qy         62 CIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKRL----MYFAYTVGLSLLT 117
               :   :|| ||    | :: :| :    :|:    : |   :|    :: :|     ||
Db         78 TVCFFHLALAD----FMLSLSLPIAMYYIVSRQWLLGEWACKLYITFVFLSYFASNCLLV 133

Qy        118 AISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEDR--- 174
              ||  ||:|||:|:|   ||    ::|:   :|        | :: ||  |||   |
Db        134 FISVDRCISVLYPVWALNHRTVQRASWLAFGVWL-------LAAALCSAHLKFRTTRKWN 186
```

```
Qy        175 -------CFRVDMVQAAL-----------------IMGVLTPVMTLSSLTLFVWVRRSSQ 210
                      |  |   | :                 ::| | |:  : :    :  :   :
Db        187 GCTHCYLAFNSDNETAQIWIEGVVEGHIIGTIGHFLLGFLGPLAIIGTCAHLIRAKLLRE 246

Qy        211 QW--RRQPTRLFVVVLASVLVFLICSLPLSIYWFVLYWLSL------PPEMQVLCFSLSR 262
               |    :| || :|::::  :|     | ::   |  |  :       | | :|     |
Db        247 GWVHANRPKRLLLVLVSAFFIFW---SPFNVVLLVHLWRRVMLKEIYHPRM-LLILQASF 302

Qy        263 LSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREEPELEG---GETP 312
                 |:|| || :|  ||     :   :|| : | :|  ||  |     |  |
Db        303 ALGCVNSSLNPFLYVFVGRDFQEKF-FQSLTSALARAFGEEEFLSSCPRGNAP 354


RESULT 15
US-08-458-970A-9
; Sequence 9, Application US/08458970A
; Patent No. 5861272
;  GENERAL INFORMATION:
;    APPLICANT:  LI, ET AL.
;    TITLE OF INVENTION:  C5a Receptor
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,970A
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09234
;      FILING DATE:  16 AUG 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-353
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  350 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-458-970A-9

  Query Match             14.5%;  Score 240.5;  DB 2;  Length 350;
  Best Local Similarity   26.8%;  Pred. No. 7.7e-14;
  Matches   84;  Conservative   55;  Mismatches  117;  Indels   57;  Gaps   12;

Qy         39 LCGMAGNSMVIWLLGFRMHRNPFCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVH 98
              | |: ||::|:|:  |    |    |: |||| || |      | |:|   |:: |:   |
Db         49 LVGVLGNALVVWVTAFEAKRTINAIWFLNLAVADFL------SCLAL---PILFTSIVQH 99

Qy         99 ----------ELMKRLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWV-CG 147
                      ::  |:       : ||  ||  | | |  ||| :  |   | ||: |
Db        100 HHWPFGGAACSILPSLILLNMYASILLLATISADRFLLVFKPIWCQNFRGAGL-AWIACA 158

Qy        148 LLWTLCLLMNGLTSSFCSKFLK------------FNEDRCFRVDMVQAALIMGVLTPVM 194
              : | | ||:     ||  : ::           :: |:     :    |::| | |::
Db        159 VAWGLALLLT--IPSFLYRVVREEYFPPPKVLCGVDYSHDKRRERAVAIVRLVLGFLWPLL 216

Qy        195 TLSSLTLFV----WVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVLYWLS-- 248
              ||:    |:    | ||:::     |:   ||:| |  | |  ||  :   :: :|
Db        217 TLTICYTFILLRTWSRRATRS-----TKTLKVVVAVVASFFIFWLPYQVTGIMMSFLEPS 271

Qy        249 -----LPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREE 303
                   |  ::  || | : ::  :    ||:|| : |     ||  :|| ::|:  | ||
Db        272 SPTFLLLNKLDSLCVSFAYINCCI----NPIIYVVAGQGFQGRL-RKSLPSLLRNVLTEE 326

Qy        304 PELEGGETPTVGT 316
                :   :: |  |
Db        327 SVVRESKSFTRST 339


Search completed: November  4, 2004, 11:06:38
Job time : 40 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 4, 2004, 10:48:33 ; Search time 40 Seconds
(without alignments)
772.140 Million cell updates/sec

Title: US-09-801-944B-268
Perfect score: 1661
Sequence: 1 MNQTLNSSGTVESALNYSRG.....EEPELEGGETPTVGTNEMGA 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	465.5	28.0	343	2	A35639	G protein-coupled
2	461	27.8	324	1	TVRTAS	transforming prote
3	438.5	26.4	325	1	TVHUAS	transforming prote
4	437	26.3	324	2	S51001	transforming prote
5	402.5	24.2	378	2	A39485	transforming prote
6	263.5	15.9	351	1	A46525	complement C5a ana
7	257.5	15.5	353	2	C42009	FMLP-related recep
8	241.5	14.5	352	1	S27357	complement C5a ana
9	240.5	14.5	350	1	A37963	complement C5a ana
10	230	13.8	371	2	JC5498	G protein-coupled
11	228	13.7	352	2	A46520	N-formyl peptide r
12	218.5	13.2	371	2	JC5796	probable chemoattr
13	214.5	12.9	364	2	A49542	N-formyl peptide c
14	208	12.5	353	2	JC2492	G protein-coupled
15	206.5	12.4	351	2	B42009	FMLP-related recep
16	202.5	12.2	391	2	A41795	somatostatin recep
17	202.5	12.2	391	2	C41795	somatostatin recep
18	202.5	12.2	391	2	A39297	somatostatin recep
19	201.5	12.1	482	2	S65766	G protein-coupled
20	196	11.8	369	2	D41795	somatostatin recep
21	195	11.7	346	2	S29248	somatostatin recep
22	193.5	11.6	346	2	JC5715	G protein-coupled
23	193	11.6	369	2	A45291	somatostatin recep
24	192	11.6	355	2	A55733	G protein-coupled
25	191.5	11.5	369	2	JC2083	somatostatin recep
26	190.5	11.5	369	2	JC5068	G protein-coupled
27	189.5	11.4	428	2	S30508	probable G protein
28	189	11.4	362	2	A39714	G protein-coupled
29	188.5	11.3	418	2	A46226	somatostatin recep
30	188	11.3	363	2	I57940	somatostatin recep
31	187.5	11.3	388	2	JN0605	somatostatin recep
32	187	11.3	350	2	A42009	N-formyl peptide r
33	186.5	11.2	359	2	A48921	interleukin-8 rece
34	186.5	11.2	369	2	B41795	somatostatin recep
35	185	11.1	362	2	A30341	G protein-coupled
36	183.5	11.0	346	2	JC5716	G protein-coupled
37	183	11.0	384	2	A47249	brain-specific som
38	182.5	11.0	428	2	A44021	somatostatin recep
39	179.5	10.8	355	2	JQ1231	interleukin-8 rece
40	179	10.8	363	2	I57955	somatostatin recep
41	179	10.8	364	2	JN0763	somatostatin recep
42	178.5	10.7	350	2	A39445	interleukin-8 rece
43	176.5	10.6	356	2	S42096	interleukin-8 rece
44	176	10.6	360	2	A53611	interleukin-8 rece
45	176	10.6	473	2	JC5835	anaphylatoxin C3a

ALIGNMENTS

RESULT 1
A35639
G protein-coupled receptor RTA - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: A35639
R;Ross, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Harcus, D.R.; Lynch, K
Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990
A;Title: RTA, a candidate G protein-coupled receptor: cloning, sequencing, and tissue di
A;Reference number: A35639; MUID:90222168; PMID:2109324
A;Accession: A35639
A;Molecule type: mRNA
A;Residues: 1-343 <ROS>
A;Cross-references: UNIPROT:P23749; GB:M35297; NID:g206809; PIDN:AAA42087.1; PID:g206810
C;Superfamily: mas transforming protein
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein
F;4/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.0%; Score 465.5; DB 2; Length 343;
Best Local Similarity 35.7%; Pred. No. 9e-33;
Matches 121; Conservative 59; Mismatches 122; Indels 37; Gaps 11;

```
Qy          2 NQTLNSSGTVESALNYSRGSTVHTAYLVLSSLA-----------MFTCLCGMAGNSMVI 49
              ||     |  |:   ||||     :| :  :|            :  ||||: || :|:
Db         13 NQNKMCPGMSEALELYSRG------FLTIEQIATLPPPAVTNYIFLLLCLCGLVGNGLVL 66

Qy         50 WLLGFRMHRNPFCIYILNLAAADLLFLFSMA--STLSLETQPLVNTTDKVHELMKRLMYF 107
              |  || : | || || |:||:|| ::||| |  : |:: |  | : | |  : : :
Db         67 WFFGFSIKRTPFSIYFLHLASADGIYLFSKAVIALLNMGTF-LGSFPDYVRRVSRIVGLC 125

Qy        108 AYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWLTLCLLMNGLTSSFCSKF 167
               :  |:||| ||| :||:||:||:|:   ||: ||| || ||| |  |:  : : ||  |
Db        126 TFFAGVSLLPAISIERCVSVIFPMWYWRRRPKRLSAGVCALLWLLSFLVTSIHNYFC-MF 184

Qy        168 L--KFNEDRCFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLA 225
              |  : :   |  :|:    |:  :  |:|  |  | | :  |   ::: |::  :|  ||||
Db        185 LGHEASGTACLNMDISLGILLFFLFCPLMVLPCLALILHVECRARR-RQRSAKLNHVVLA 243

Qy        226 SVLVFLICSLPLSIYWFVLYWLSLP---PEMQVLCFSLSRLSSSVSSSANPVIYFLVGSR 282
              | |||: |: | | ||: :  :|   ||      :: |   ::||| |::||| |
Db        244 IVSVFLVSSIYLGIDWFLFWVFQIPAPFPEY------VTDLCICINSSAKPIVYFLAGRD 297

Qy        283 RSHRLPTRSLGTVLQQALRE--EPELEGGETPTVGTNEM 319
              :| ||    |  | |:|||:  ||       ||   | ||
Db        298 KSQRL-WEPLRVVFQRALRDGAEPGDAASSTPNTVTMEM 335
```

RESULT 2
TVRTAS
transforming protein mas - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004

```
C;Accession: A31816
R;Young, D.; O'Neill, K.; Jessell, T.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 5339-5342, 1988
A;Title: Characterization of the rat mas oncogene and its high-level expression in the h
A;Reference number: A31816; MUID:88276953; PMID:2455902
A;Accession: A31816
A;Molecule type: mRNA
A;Residues: 1-324 <YOU>
A;Cross-references: UNIPROT:P12526; GB:J03823; NID:g205313; PIDN:AAA41573.1; PID:g205314
C;Genetics:
A;Gene: mas
C;Superfamily: mas transforming protein
C;Keywords: G protein-coupled receptor; transforming protein; transmembrane protein
F;31-47/Domain: transmembrane #status predicted <TM1>
F;72-88/Domain: transmembrane #status predicted <TM2>
F;149-165/Domain: transmembrane #status predicted <TM3>
F;185-204/Domain: transmembrane #status predicted <TM4>
F;225-243/Domain: transmembrane #status predicted <TM5>

  Query Match             27.8%;  Score 461;  DB 1;  Length 324;
  Best Local Similarity   33.9%;  Pred. No. 2.1e-32;
  Matches  114;  Conservative   64;  Mismatches  118;  Indels   40;  Gaps   10;

Qy          1 MNQTLNSSGTVESALNYSRGS----TVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRM 56
              |:|:  :|   | |:| |  :    | |    ::  : |     |   | :::| | |||
Db          1 MDQSNMTSFAEEKAMNTSSRNASLGTSHPPIPIVHWVIMSISPLGFVENGILLWFLCFRM 60

Qy         57 HRNPFCIYILNLAAADL-----LFLFSMASTLSLE-------TQPLVNTTDKVHELMKRL 104
               |||| :|| :|: ||:     :|: |:   |  |       |   :: |
Db         61 RRNPFTVYITHLSIADISLLFCIFILSIDYALDYELSSGHYYTIVTLSVT---------- 110

Qy        105 MYFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFC 164
              | |  || |||||| :||||||:|||::||||:| ||:|| ||| |  |:  :    |
Db        111 FLFGYNTGLYLLTAISVERCLSVLYPIWYRCHRPKHQSAFVCALLWALSCLVTTMEYVMC 170

Qy        165 --SKFLKFNEDRCFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVV 222
                |      ::  |  | :  | |    | ||:| :||  | | :|::  |    ::|::|
Db        171 IDSGEESHSQSDCRAVIIFIAILSFLVFTPLMLVSSTILVVKIRKNT--WASHSSKLYIV 228

Qy        223 VLASVLVFLICSLPLSIYWFVL--YWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVG 280
              :: ::::||| ::|: : : :   || :          ::| | |:::||||| ||| ||
Db        229 IMVTIIIFLIFAMPMRVLYLLYYEYWSTFGN-----LHNISLLFSTINSSANPFIYFFVG 283

Qy        281 SRRSHRLPTRSLGTVLQQALREE--PELEGGETPTV 314
              | :  |    ||  || :| ::|  |  : |   ||
Db        284 SSKKKRF-RESLKVVLTRAFKDEMQPRRQEGNGNTV 318


RESULT 3
TVHUAS
transforming protein mas - human
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A01375
R;Young, D.; Waitches, G.; Birchmeier, C.; Fasano, O.; Wigler, M.
Cell 45, 711-719, 1986
A;Title: Isolation and characterization of a new cellular oncogene encoding a protein wi
A;Reference number: A01375; MUID:86218084; PMID:3708691
A;Accession: A01375
A;Molecule type: DNA
A;Residues: 1-325 <YOU>
A;Cross-references: UNIPROT:P04201; GB:M13150; NID:g187388; PIDN:AAA36199.1; PID:g307158
C;Genetics:
A;Gene: GDB:MAS1
A;Cross-references: GDB:120166; OMIM:165180
A;Map position: 6q24-6q27
C;Superfamily: mas transforming protein
C;Keywords: G protein-coupled receptor; glycoprotein; proto-oncogene; transforming prote
F;31-61/Domain: transmembrane #status predicted <TM1>
F;66-97/Domain: transmembrane #status predicted <TM2>
F;105-135/Domain: transmembrane #status predicted <TM3>
F;150-172/Domain: transmembrane #status predicted <TM4>
F;186-214/Domain: transmembrane #status predicted <TM5>
F;225-250/Domain: transmembrane #status predicted <TM6>
F;258-286/Domain: transmembrane #status predicted <TM7>
F;5,16,22,272/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             26.4%;  Score 438.5;  DB 1;  Length 325;
  Best Local Similarity   33.6%;  Pred. No. 1.9e-30;
  Matches  107;  Conservative   58;  Mismatches  114;  Indels   39;  Gaps    9;

Qy          7 SSGTVESALNYSRG-----STVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPF 61
              :|  ||   | | |         |    ::  : |      |   | :::| | ||| ||||
Db          7 TSFVVEEPTNISTGRNASVGNAHRQIPIVHWVIMSISPVGFVENGILLWFLCFRMRRNPF 66

Qy         62 CIYILNLAAADL-----LFLFSMASTLSLE-------TQPLVNTTDKVHELMKRLMYFAY 109
               :|| :|: ||:     :|: |:   |  |       |   :: |           | |
Db         67 TVYITHLSIADISLLFCIFILSIDYALDYELSSGHYYTIVTLSVT----------FLFGY 116

Qy        110 TVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLK 169
               || |||||| :||||||:|||::||||:: || || ||| |  |:  :    |     :
Db        117 NTGLYLLTAISVERCLSVLYPIWYRCHRPKYQSALVCALLWALSCLVTTMEYVMCIDREE 176

Qy        170 FNEDR--CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASV 227
               :  |  |  | :  | |   | ||:| :||  | | :|::  |    ::|::|:: ::
Db        177 ESHSRNDCRAVIIFIAILSFLVFTPLMLVSSTILVVKIRKNT--WASHSSKLYIVIMVTI 234

Qy        228 LVFLICSLPLSIYWFVL--YWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSH 285
              ::||| ::|: : : :   || :          :| | |:::||||| ||| ||| :
Db        235 IIFLIFAMPMRLLYLLYYEYWSTFGN-----LHHISLLFSTINSSANPFIYFFVGSSKKK 289

Qy        286 RLPTRSLGTVLQQALREE 303
              |    ||  || :| ::|
Db        290 RF-KESLKVVLTRAFKDE 306


RESULT 4
S51001
transforming protein mas - mouse
N;Alternate names: mas proto-oncogene protein; probable G protein-coupled receptor mas
C;Species: Mus musculus (house mouse)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S51001; I48647; S29619
R;Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.
FEBS Lett. 357, 27-32, 1995
A;Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral t
A;Reference number: S51001; MUID:95094925; PMID:8001672
A;Accession: S51001
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-324 <MET>
A;Cross-references: UNIPROT:P30554; EMBL:X67735
R;Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.
FEBS Lett. 357, 27-32, 1995
A;Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral t
A;Reference number: I48647; MUID:95094925; PMID:8001672
A;Accession: I48647
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-87,'I',89-324 <RES>
A;Cross-references: EMBL:X67735; NID:g53011; PIDN:CAA47964.1; PID:g53012
C;Genetics:
A;Gene: mas
C;Superfamily: mas transforming protein
C;Keywords: G protein-coupled receptor; proto-oncogene; transmembrane protein

  Query Match             26.3%;  Score 437;  DB 2;  Length 324;
  Best Local Similarity   33.8%;  Pred. No. 2.5e-30;
  Matches  116;  Conservative   61;  Mismatches  112;  Indels   54;  Gaps   12;

Qy          1 MNQTLNSSGTVESALNYSR-----GST------VHTAYLVLSSLAMFTCLCGMAGNSMVI 49
              |:|:  :|   | |:| |       ||:      ||   : :| |         |   | :::
Db          1 MDQSNMTSLAEEKAMNTSSRNASLGSSHPPIPIVHWVIMSISPL-------GFVENGILL 53

Qy         50 WLLGFRMHRNPFCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKV--HELMKRLMY- 106
               | | ||| |||| :|| :|: ||:  || :           : :||    :||     |
```

```
Db          54 WFLCFRMRRNPFTVYITHLSMADISLLFCI----------FILSTDYALDYELSSGHHYT 103

Qy         107 ---------FAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMN 157
                       | |  || |||||| :||||||:|||:  |||:| ||:|| ||  |  |:
Db         104 IVTLSVTFLFGYNTGLYLLTAISVERCLSVLYPIWYTSHRPKHQSAFVCALLCALSCLVT 163

Qy         158 GLTSSFCSKFLKFNEDR--CFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQ 215
               :   |      : :  |  |  | :  | |    | ||:| :||  | | :|::  |
Db         164 TMEYVMCIDSGEESHSRSDCRAVIIFIAILSFLVFTPLMLVSSSILVVKIRKNT--WASH 221

Qy         216 PTRLFVVVLASVLVFLICSLPLSIYWFVL--YWLSLPPEMQVLCFSLSRLSSSVSSSANP 273
               ::|::|:: :::::||| ::|: : : :    || :          ::| | |:::|||||
Db         222 SSKLYIVIMVTIIIFLIFAMPMRVLYLLYYEYWSAFGN-----LHNISLLFSTINSSANP 276

Qy         274 VIYFLVGSRRSHRLPTRSLGTVLQQALREE--PELEGGETPTV 314
               ||| ||| :  |    ||  || :| ::|  |  : |   ||
Db         277 FIYFFVGSSKKKRF-RESLKVVLTRAFKDEMQPRRQEGNGNTV 318


RESULT 5
A39485
transforming protein (mrg) - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A39485
R;Monnot, C.; Weber, V.; Stinnakre, J.; Bihoreau, C.; Teutsch, B.; Corvol, P.; Clauser,
Mol. Endocrinol. 5, 1477-1487, 1991
A;Title: Cloning and functional characterization of a novel mas-related gene, modulating
A;Reference number: A39485; MUID:92130997; PMID:1723144
A;Accession: A39485
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <MON>
A;Cross-references: UNIPROT:P35410; GB:S78653; NID:g244209; PIDN:AAB21255.1; PID:g244210
C;Superfamily: mas transforming protein
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             24.2%;  Score 402.5;  DB 2;  Length 378;
  Best Local Similarity   36.1%;  Pred. No. 2.8e-27;
  Matches  110;  Conservative   50;  Mismatches  102;  Indels   43;  Gaps    9;

Qy          29 VLSSLAMFTCLCGMAGNSMVIWLL--GFRMHRNPFCIYILNLAAADLLFL-FSMASTLSL 85
               :::  |:   |||:  | | ||| |     ||: :|||:| |||:::|  |    | :
Db          77 IIAPKAVLVSLCGVLLNGTVFWLLCCG---ATNPYMVYILHLVAADVIYLCCSAVGFLQV 133

Qy          86 ETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWV 145
                     : : :  |  |:: | | || ||||:||: |||||::|||:: | |
Db         134 TLLTYHGVVFFIPDFLAILSPFSFEVCLCLLVAISTERCVCVLFPIWYRCHRPKYTSNVV 193

Qy         146 CGLLWTLCLLMNGLTSSF---------CSKFLKFNEDRCFRVDMVQAALIMGVLTPVMTL 196
               | |:| |   :| : | |          |  |||             : |   :|: || :
Db         194 CTLIWGLPFCINIVKSLFLTYWKHVKACVIFLKL-----------SGLFHAILSLVMCV 241

Qy         197 SSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVLYWLSLPPEMQVL 256
               ||||| :     |||  :: ||:: ||  |  :|: :||||:  :  :    :|
Db         242 SSLTLLIRFLCCSQQ--QKATRVYAVVQISAPMFLLWALPLSVAPLITDF---KMFVT 294

Qy         257 CFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREEPELEGGETPTVGT 316
               |  |  ::|||||:||| ||| |  ||  ||  :||:|| ::||         ||
Db         295 TSYLISLFLIINSSANPIIYFFVGSLRKKRL-KESLRVILQRALADKPE--------VGR 345

Qy         317 NEMGA 321
               |:  |
Db         346 NKKAA 350


RESULT 6
A46525
complement C5a anaphylatoxin receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A46525
R;Gerard, C.; Bao, L.; Orozco, O.; Pearson, M.; Kunz, D.; Gerard, N.P.
J. Immunol. 149, 2600-2606, 1992
A;Title: Structural diversity in the extracellular faces of peptidergic G-protein-coupled
A;Reference number: A46525; MUID:93017861; PMID:1401897
A;Accession: A46525
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-351 <GER>
A;Cross-references: GB:S46665; GB:L05630; NID:g257519; PIDN:AAB97774.1; PID:g257520
A;Experimental source: BALB/C
A;Note: sequence extracted from NCBI backbone (NCBIP:116075)
C;Function:
A;Description: mediates the inflammatory and chemotactic responses of polymorphonuclear r
n
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorph
F;1-37/Domain: extracellular #status predicted <EX1>
F;38-61/Domain: transmembrane #status predicted <TM1>
F;62-71/Domain: intracellular #status predicted <IN1>
F;72-94/Domain: transmembrane #status predicted <TM2>
F;95-110/Domain: extracellular #status predicted <EX2>
F;111-132/Domain: transmembrane #status predicted <TM3>
F;133-149/Domain: intracellular #status predicted <IN2>
F;150-174/Domain: transmembrane #status predicted <TM4>
F;175-207/Domain: extracellular #status predicted <EX3>
F;208-228/Domain: transmembrane #status predicted <TM5>
F;229-243/Domain: intracellular #status predicted <IN3>
F;244-265/Domain: transmembrane #status predicted <TM6>
F;266-284/Domain: extracellular #status predicted <EX4>
F;285-308/Domain: transmembrane #status predicted <TM7>
F;309-351/Domain: intracellular #status predicted <IN4>
F;6/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             15.9%;  Score 263.5;  DB 1;  Length 351;
  Best Local Similarity   28.0%;  Pred. No. 2.8e-15;
  Matches   92;  Conservative   54;  Mismatches  122;  Indels   61;  Gaps   14;

Qy          26 AYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIYILNLAAADLLFLFSMASTLSL 85
               | |:: |:     | |: ||::|:|:  |        |: |||| ||||   :|
Db          39 AALIIYSVVF---LVGVPGNALVVWVTAFEPDGPSNAIWFLNLAVADLLSCLAM------ 89

Qy          86 ETQPLVNTTDKVHE----------LMKRLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKC 135
                  |:: ||   |            ::  |:        : ||  || | | |  ||| |
Db          90 ---PVLFTTVLNHNYWYFDATACIVLPSLILLNMYASILLLATISADRFLLVFKPIW--C 144

Qy         136 HRPRHLS-AWV-CGLLWTLCLLMNGLTSSFCSKFLKFNEDR----------CFRVDMVQA 183
               : |    ||: ||: | | ||:   :  :   :  | :             |  :   |
Db         145 QKVRGTGLAWMACGVAWVLALLLTIPSFVYREAYKDFYSEHTVCGINYGGGSFPKEKAVA 204

Qy         184 --ALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTR---LFVVVLASVLVFLICSLPLS 238
                  |::| : |::||:     |: :|      | |: ||       ||:| |: | |  ||
Db         205 ILRLMVGFVLPLLTLNICYTFLLLR----TWSRKATRSTKTLKVVMAVVICFFIFWLPYQ 260

Qy         239 IYWFVLYWLSLPP---------EMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPT 289
               :   :: |  |||           ::  || ||: ::  |    ||:|| : |     ||
Db         261 VTGVMIAW--LPPSSPTLKRVEKLNSLCVSLAYINCCV----NPIIYVMAGQGFHGRL-L 313

Qy         290 RSLGTVLQQALREEPELEGGETPTVGTNE 318
               ||| :::: || |:       :| |  |::
Db         314 RSLPSIIRNALSEDSVGRDSKTFTPSTDD 342


RESULT 7
C42009
FMLP-related receptor 2 - human
N;Alternate names: FMLP-related receptor I; probable chemotactic receptor FPRH2
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: C42009
R;Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
Genomics 13, 437-440, 1992
A;Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR), a
A;Reference number: A42009; MUID:92307681; PMID:1612600
A;Accession: C42009
```

A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-353 <BAO>
A;Cross-references: UNIPROT:P25089; GB:M76673; NID:g182668; PID:g182669
C;Comment: This fMet-Leu-Phe receptor homolog, whose ligand is not yet known, appears nc
C;Genetics:
A;Gene: GDB:FPRL2
A;Cross-references: GDB:128855; OMIM:136539
A;Map position: 19q13.3-19q13.4
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 15.5%; Score 257.5; DB 2; Length 353;
Best Local Similarity 28.6%; Pred. No. 9.2e-15;
Matches 91; Conservative 48; Mismatches 134; Indels 45; Gaps 14;

```
Qy         24 HTAYLVLSSLAM-FTCLCGMAGNSMVIWLLGFRMHRNPFCIYILNLAAADLLFL----FS 78
              ||    : | |     | : |: || :|||: |||| |     |  |||| ||  |      |
Db         22 HTVLWIFSLLVHGVTPVFGVLGNGLVIWVAGFRMTRTVNTICYLNLALADFSFSAILPFR 81

Qy         79 MASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRP 138
              | |     |  |   :  |: :|  :  |   | : |:| |:  ||: || | | : ||
Db         82 MVSVAMREKWPFASPLCKLVHVMIDINLF---VSVYLITIIALDRCICVLHPAWAQNHRT 138

Qy        139 RHLS------AWVCGLL--------WTLCLLMNGLTSSFCSKFLKFNEDRCFR-----VD 179
               |:       |:  ::         ||     ||   ::|     |  |          :
Db        139 MSLAKRVMTGLWIFTIVLTLPNFIFWTTISTTNG--DTYCIFNFAFWGDTAVERLNVFIT 196

Qy        180 MVQAALIM----GVLTP--VMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLIC 233
              | :  ||:     |  | ::|:    :   : |:       :| |:|  |:||   | ||
Db        197 MAKVFLILHFIIGFTVPMSIITVCYGIIAAKIHRNHMIKSSRPLRVFAAVVAS---FFIC 253

Qy        234 SLPLSIYWFVL-YWLS---LPPEMQVLCFSLSRLSSSV--SSSANPVIYFLVGSRRSHRL 287
                |  :   ::  ||    |  : :::   ::  ||    :|  ||::|  :|     ||
Db        254 WFPYELIGILMAVWLKEMLLNGKYKIILVLINPTSSLAFFNSCLNPILYVFMGRNFQERL 313

Qy        288 PTRSLGTVLQQALREEPE 305
                |||  | |::|| | |:
Db        314 -IRSLPTSLERALTEVPD 330
```

RESULT 8
S27357
complement C5a anaphylatoxin receptor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S27357
R;Perret, J.J.; Raspe, E.; Vassart, G.; Parmentier, M.
Biochem. J. 288, 911-917, 1992
A;Title: Cloning and functional expression of the canine anaphylatoxin C5a receptor. Evi
A;Reference number: S27357; MUID:93111969; PMID:1472004
A;Accession: S27357
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352 <PER>
A;Cross-references: UNIPROT:P30992; EMBL:X65860; NID:g878; PIDN:CAA46690.1; PID:g879
C;Function:
A;Description: mediates the inflammatory and chemotactic responses of polymorphonuclear
n
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorp
F;1-38/Domain: extracellular #status predicted <EX1>
F;39-62/Domain: transmembrane #status predicted <TM1>
F;63-72/Domain: intracellular #status predicted <IN1>
F;73-95/Domain: transmembrane #status predicted <TM2>
F;96-111/Domain: extracellular #status predicted <EX2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;134-150/Domain: intracellular #status predicted <IN2>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;176-208/Domain: extracellular #status predicted <EX3>
F;209-229/Domain: transmembrane #status predicted <TM5>
F;230-244/Domain: intracellular #status predicted <IN3>
F;245-266/Domain: transmembrane #status predicted <TM6>
F;267-285/Domain: extracellular #status predicted <EX4>
F;286-309/Domain: transmembrane #status predicted <TM7>
F;310-352/Domain: intracellular #status predicted <IN4>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 241.5; DB 1; Length 352;
Best Local Similarity 26.2%; Pred. No. 2.2e-13;
Matches 90; Conservative 58; Mismatches 146; Indels 49; Gaps 11;

```
Qy          4 TLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCI 63
              ||: :  |: :||  : |      ||:  :     | |: || :|:|: || : |    |
Db         18 TLDPNIFVDESLNTPKLSVPDMIALVIFVMVF---LVGVPGNFLVVWVTGFEVRRTINAI 74

Qy         64 YILNLAAADLLFLFSMASTLSLETQ----PLVNTTDKVHELMKRLMYFAYTVGLSLLTAI 119
              : |||| ||||   ::    |   |     | |   ::   :  |:       : ||| |
Db         75 WFLNLAVADLLSCLALPILFSSIVQQGYWPFGNAACRI---LPSLILLLNMYASILLLTTI 131

Qy        120 STQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLM-------NGLTSSFCSKFLKFNE 172
              | | : |  ||| : :|   |:   | : | : ||:        |: : :   ::
Db        132 SADRFVLVFNPIWCQNYRGPQLAWAACSVAWAVALLLTVPSFIFRGVHTEYFPFWMTCGV 191

Qy        173 DRCFRVDMVQAA-----LIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTR---LFVVVL 224
              |     :|:        |:|| | |:: ||     |: :|      | |: ||       ||:
Db        192 DYSGVGVLVERGVAILRLLMGFLGPLVILSICYTFLLIR---TWSRKATRSTKTLKVVV 247

Qy        225 ASVLVFLICSLPLSIYWFVLYWLSLPPE-------MQVLCFSLSRLSSSVSSSANPVIYF 277
              | |: | :  ||  :   ::        |       :  || ::: ::  :    ||:||
Db        248 AVVVSFFVLWLPYQVTGMMMALFYKHSESFRRVSRLDSLCVAVAYINCCI----NPIIYV 303

Qy        278 LVG----SRRSHRLPTRSLGTVLQQALREEPELEGGETPTVGT 316
              |      ||    || |     |:| | ||       :: |: |
Db        304 LAAQGFHSRFLKSLPAR-----LRQVLAEESVGRDSKSITLST 341
```

RESULT 9
A37963
complement C5a anaphylatoxin receptor - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: A37963; S13646; I52417; S30518
R;Boulay, F.; Mery, L.; Tardif, M.; Brouchon, L.; Vignais, P.
Biochemistry 30, 2993-2999, 1991
A;Title: Expression cloning of a receptor for C5a anaphylatoxin on differentiated HL-60 c
A;Reference number: A37963; MUID:91175748; PMID:2007135
A;Accession: A37963
A;Molecule type: mRNA
A;Residues: 1-350 <BOU>
A;Cross-references: UNIPROT:P21730; GB:J05327; NID:g179699; PIDN:AAA62831.1; PID:g179700
R;Gerard, N.P.; Gerard, C.
Nature 349, 614-617, 1991
A;Title: The chemotactic receptor for human C5a anaphylatoxin.
A;Reference number: S13646; MUID:91156029; PMID:1847994
A;Accession: S13646
A;Molecule type: mRNA
A;Residues: 1-350 <GER>
A;Cross-references: EMBL:X58674; NID:g29568; PIDN:CAB37830.1; PID:g4467832
R;Gerard, N.P.; Bao, L.; Xiao-Ping, H.; Eddy, R.L.
Biochemistry 32, 1243-1250, 1993
A;Title: Human chemotaxis receptor genes cluster at 19q13.3-13.4. Characterization of the
A;Reference number: I52417; MUID:93192225; PMID:8383526
A;Accession: I52417
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3 <RES>
A;Cross-references: GB:S56556; GB:S56557; NID:g298577; NID:g298578
C;Genetics:
A;Gene: GDB:C5R1; C5A; C5AR
A;Cross-references: GDB:128856; OMIM:113995
A;Map position: 19q13.3-19q13.4
A;Introns: 1/3
A;Note: the list of introns may be incomplete
C;Function:

```
A;Description: mediates the inflammatory and chemotactic responses of polymorphonuclear
n
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorp
F;1-37/Domain: extracellular #status predicted <EX1>
F;38-61/Domain: transmembrane #status predicted <TM1>
F;62-71/Domain: intracellular #status predicted <IN1>
F;72-94/Domain: transmembrane #status predicted <TM2>
F;95-110/Domain: extracellular #status predicted <EX2>
F;111-132/Domain: transmembrane #status predicted <TM3>
F;133-149/Domain: intracellular #status predicted <IN2>
F;150-174/Domain: transmembrane #status predicted <TM4>
F;175-206/Domain: extracellular #status predicted <EX3>
F;207-227/Domain: transmembrane #status predicted <TM5>
F;228-242/Domain: intracellular #status predicted <IN3>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;265-283/Domain: extracellular #status predicted <EX4>
F;284-307/Domain: transmembrane #status predicted <TM7>
F;308-350/Domain: intracellular #status predicted <IN4>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            14.5%;  Score 240.5;  DB 1;  Length 350;
  Best Local Similarity   26.8%;  Pred. No. 2.7e-13;
  Matches   84;  Conservative   55;  Mismatches  117;  Indels   57;  Gaps   12;

Qy         39 LCGMAGNSMVIWLLGFRMHRNPFCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVH 98
Db         49 LVGVLGNALVVWVTAFEAKRTINAIWFLNLAVADFL------SCLAL---PILFTSIVQH 99

Qy         99 ----------ELMKRLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWV-CG 147
Db        100 HHWPFGGAACSILPSLILLNMYASILLLATISADRFLLVFKPIWCQNFRGAGL-AWIACA 158

Qy        148 LLWTLCLLMNGLTSSFCSKFLK------------FNEDRCFRVDMVQAALIMGVLTPVM 194
Db        159 VAWGLALLLT--IPSFLYRVVREEYFPPKVLCGVDYSHDKRRERAVAIVRLVLGFLWPLL 216

Qy        195 TLSSLTLFV----WVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVLYWLS-- 248
Db        217 TLTICYTFILLRTWSRRATRS-----TKTLKVVVAVVASFFIFWLPYQVTGIMMSFLEPS 271

Qy        249 -----LPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREE 303
Db        272 SPTFLLLNKLDSLCVSFAYINCCI----NPIIYVVAGQGFQGRL-RKSLPSLLRNVLTEE 326

Qy        304 PELEGGETPTVGT 316
Db        327 SVVRESKSFTRST 339


RESULT 10
JC5498
G protein-coupled receptor DEZ - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: JC5498
R;Methner, A.; Hermey, G.; Schinke, B.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 233, 336-342, 1997
A;Title: A novel G protein-coupled receptor with homology to neuropeptide and chemoattra
A;Reference number: JC5498; MUID:97289630; PMID:9144535
A;Contents: Brain
A;Accession: JC5498
A;Molecule type: mRNA
A;Residues: 1-371 <MET>
A;Cross-references: UNIPROT:P97468; GB:U79525; NID:g1732346; PIDN:AAB53789.1; PID:g17323
C;Comment: This protein is involved in the bone metabolism.
C;Superfamily: vertebrate rhodopsin
F;110-187/Disulfide bonds: #status predicted

  Query Match            13.8%;  Score 230;  DB 2;  Length 371;
  Best Local Similarity   21.5%;  Pred. No. 2.3e-12;
  Matches   82;  Conservative   62;  Mismatches  148;  Indels   90;  Gaps   11;

Qy          6 NSSGTVESALNYSRG----------STVHTAYLVLSSLAMFTCLCGMAGNSMVIWL 51
Db          7 NDSGIYDD--EYSDGFGYFVDLEEASPWEAKVAPVFLVV--IYSLVCFLGLLGNGLVIVI 62

Qy         52 LGFRMHRNPFCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKV-----HELMKRLMY 106
Db         63 ATFKMKKTVNTVWFVNLAVADFLFNIFLPMHITYAAMDYHWVFGKAMCKISNFLLSHNMY 122

Qy        107 FAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSK 166
Db        123 ----TSVFLLTVISFDRCISVLLPVWSQNHRSIRLAYMTCSAVWVLAFFLSSPSLVFRDT 178

Qy        167 FLKFNEDRCF-------------------------RVDMVQAALIMGVLTPVMTLSS-- 198
Db        179 ANIHGKITCFNNFSLAAPESSPHPAHSQVVSTGYSRHVAVTVTRFLCGFLIPVFIITACY 238

Qy        199 LTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPL-SIYWFVLYWLSLPPEMQVLC 257
Db        239 LTIVFKLQRNRLAKNKKP---FKIIITIIITFFLCWCPYHTLYLLELHHTAVPSSVFSLG 295

Qy        258 FSLSRLSSSVSSSANPVIYFLVG-------------------------SRRSHRLPTRSL 292
Db        296 LPLATAVAIANSCMNPILYVFMGHDFRKFKVALFSRLANALSEDTGPSSYPSHRSFTK-- 353

Qy        293 GTVLQQALREEPELEGGETPTV 314
Db        354 ----MSSLNEKASVNEKETSTL 371


RESULT 11
A46520
N-formyl peptide receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46520
R;Ye, R.D.; Quehenberger, O.; Thomas, K.M.; Navarro, J.; Cavanagh, S.L.; Prossnitz, E.R.;
J. Immunol. 150, 1383-1394, 1993
A;Title: The rabbit neutrophil N-formyl peptide receptor. cDNA cloning, expression, and s
A;Reference number: A46520; MUID:93163563; PMID:8432984
A;Accession: A46520
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-352 <YE1>
A;Cross-references: UNIPROT:Q05394; GB:M94549; NID:g165027; PIDN:AAA31254.1; PID:g165028
A;Experimental source: NZW, neutrophils
A;Note: sequence extracted from NCBI backbone (NCBIP:124908)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match            13.7%;  Score 228;  DB 2;  Length 352;
  Best Local Similarity   26.7%;  Pred. No. 3.3e-12;
  Matches   94;  Conservative   58;  Mismatches  138;  Indels   62;  Gaps   16;

Qy         15 LNYSRGSTVHTAYLVLSS-----LAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIYILNLA 69
Db          9 LNVSGGTQATPAGLVVLDVFSYLILVVTFVLGVLGNGLVIWVTGFRMTHTVTTISYLNLA 68

Qy         70 AADLLFLFSMASTLS--LETQPLVNTTDKVHELMKRLMYFAYTV-------GLSLLTAIS 120
Db         69 LAD----FSFTSTLPFFIVTKALGGHWPFGWFLCK----FVFTIVDINLFGSVFLIALIA 120

Qy        121 TQRCLSVLFPIWFKCHRPRHLS------AWVCGLLWTLCLLMNGLTSSF--------CS- 165
Db        121 LDRCICVLHPVWAQNHRNVSLAKKVIVGPWICALLLTLPVIIRVTTLSHPRAPGKMACTF 180

Qy        166 KFLKFNEDRCFRVD------MVQAAL--IMGVLTP--VMTLSSLTLFVWVRRSSQQWRRQ 215
Db        181 DWSPWTEDPAEKLKVAISMFMVRGIIRFIIGFSTPMSIVAVCYGLIATKIHRQGLIKSSR 240

Qy        216 PTRLFVVVLASVLVFLICSLPLSIYWFVL------YWLSLPPEMQVLCFSLSRLSSSVSS 269
Db        241 PLRVLSFVVAS---FLLCWSPYQIAALIATVRIRELLLGMGKDLRIV-LDVTSFVAFFNS 296
```

```
Qy        270 SANPVIYFLVGSRRSHRLPTRSLGTVLQQALREEPELEGGETPTVGTNEMGA 321
              ||::|  :|     ||   ||   |::|| |    :  :|   |||   |
Db        297 CLNPMLYVFMGQDFRERL-IHSLPASLERALSE----DSAQTSDTGTNSTSA 343
```

RESULT 12
JC5796
probable chemoattractant receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JC5796
R;Owman, C.; Lolait, S.J.; Santen, S.; Olde, B.
Biochem. Biophys. Res. Commun. 241, 390-394, 1997
A;Title: Molecular cloning and tissue distribution of cDNA encoding a novel chemoattract
A;Reference number: JC5796; MUID:98086361; PMID:9425281
A;Accession: JC5796
A;Molecule type: mRNA
A;Residues: 1-371 <OWM>
A;Cross-references: UNIPROT:O35786; DDBJ:AJ002745; NID:g2624397; PIDN:CAA05715.1; PID:g2
A;Experimental source: liver
C;Comment: This protein regulates the trafficking of immune cells during a microbial cha
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; receptor; transmembrane protein
F;39-62/Domain: transmembrane #status predicted <TM1>
F;74-94/Domain: transmembrane #status predicted <TM2>
F;112-135/Domain: transmembrane #status predicted <TM3>
F;156-177/Domain: transmembrane #status predicted <TM4>
F;206-237/Domain: transmembrane #status predicted <TM5>
F;259-280/Domain: transmembrane #status predicted <TM6>
F;302-317/Domain: transmembrane #status predicted <TM7>
F;7,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match 13.2%; Score 218.5; DB 2; Length 371;
  Best Local Similarity 22.0%; Pred. No. 2.3e-11;
  Matches 79; Conservative 65; Mismatches 140; Indels 75; Gaps 11;

```
Qy          5 LNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIY 64
              |  :| :|: :          | : |  :   |  |: || :|| :  |:| :    ::
Db         26 LEEAGPLEAKV----------AEVFLVVIYSLVCFLGILGNGLVIVIATFKMKKTVNTVW 75

Qy         65 ILNLAAADLLFLFSMASTLSLETQP----LVNTTDKVHELMKRLMYFAYTVGLSLLTAIS 120
               :||| || ||   :   ::                |:   :  | :  ||  : ||| ||
Db         76 FVNLAVADFLFNIFLPIHITYAAMDYHWVFGKAMCKISSFL--LSHNMYT-SVFLLTVIS 132

Qy        121 TQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLC------LLMNGLTSSFCSKFLKFNE-- 172
              ||:||| |:| : ||   |:   | ::|          |: |  |:   |   ||
Db        133 FDRCISVLLPVWSQNHRSVRLAYMTCVVVWVWLSSESPPSLVFGHVSTSHGKITCFNNFS 192

Qy        173 ------------------DRCFRVDMVQAALIMGVLTPVMTLSS--LTLFVWVRRSSQQW 212
                               | :    : | | ||  :::  ||:   ::|: |
Db        193 LAAPEPFSHSTHPRTDPVGYSRHVAVTVTRFLCGFLIPVFIITACYLTIVFKLQRNRQAK 252

Qy        213 RRQPTRLFVVVLASVLVFLICSLPL-SIYWFVLYWLSLPPEMQVLCFSLSRLSSSVSSSA 271
              ::|   | :::  :: | :|  |  ::|  |:  ::|  :  |  |:  :  :|
Db        253 TKKP---FKIIITIIIITFFLCWCPYHTLYLLELHHTAVPASVFSLGLPLATAVAIANSCM 309

Qy        272 NPVIYFLVG------------------------SRRSHRLPTRSLGTVLQQALREEPE 305
              ||::|  :|                       |  |||  |: : :::::|   | |
Db        310 NPILYVFMGHDFKKFKVALFSRLVNALSEDTGPSSYPSHRSFTK-MSSLIEKASVNEKE 367
```

RESULT 13
A49542
N-formyl peptide chemotactic receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A49542
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 268, 25395-25401, 1993
A;Title: Species and subtype variants of the N-formyl peptide chemotactic receptor revea
A;Reference number: A49542; MUID:94064602; PMID:8244972
A;Accession: A49542
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-364 <GAO>
A;Cross-references: UNIPROT:P33766; GB:L22181; NID:g347396; PIDN:AAA16110.1; PID:g347397
C;Genetics:
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; transmembrane protein

  Query Match 12.9%; Score 214.5; DB 2; Length 364;
  Best Local Similarity 25.8%; Pred. No. 5e-11;
  Matches 96; Conservative 56; Mismatches 137; Indels 83; Gaps 18;

```
Qy          2 NQTLNSSGTVESALNYSRGST--VHTAYLVLS--SLAMF--TCLCGMAGNSMVIWLLGFR 55
              | :|  : :  : :| | |||  |   |:||  |  :|  | : |: || :||| |||
Db          4 NMSLLMNKSAVNLMNVS-GSTQSVSAGYIVLDVFSYLIFAVTFVLGVLGNGLVIWVAGFR 62

Qy         56 MHRNPFCIYILNLAAADLLFLFSMASTLSLETQPLVNTTDKVHELMKR-------LMYFA 108
              |      | |||| ||    |   |||      :|         |              :  |
Db         63 MKHTVTTISYLNLAIAD----FCFTSTLPFYIASMV---------MGGHWPFGWFMCKFI 109

Qy        109 YTV-------GLSLLTAISTQRCLSVLFPIWFKCHRPRHLS------AWVCGLLWTLCLL 155
              |||       : |:  |:  ||: || |:| : ||   |:       |:|  | || ::
Db        110 YTVIDINLFGSVFLIALIALDRCICVLHPVWAQNHRTVSLAKKVIIVPWICAFLLTLPVI 169

Qy        156 MN---------GLTSSFCS-KFLKFNED----RCFRVDMVQA----ALIMGVLTPVMTLS 197
              :         |   : |:  |  : :|    |   | |:        |:|  || |::
Db        170 IRLTTVPNSRLGPGKTACTFDFSPWTKDPVEKRKVAVTMLTVRGIIRFIIGFSTP-MSIV 228

Qy        198 SLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVLYWLSLPPEMQ--- 254
              ::   :   : :|   : :|   |:   |  | :|  |  :         ::|   :|
Db        229 AICYGLITTKIHRQGLIKSSRPLRVLSFVVAAFFLCWCPFQV-------VALISTIQVRE 281

Qy        255 ---------VLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREEPE 305
                      |    ::   :  :|  ||::|  :|     ||   ||   |::|| |
Db        282 RLKNMTPGIVTALKITSPLAFFNSCLNPMLYVFMGQDFRERL-IHSLPASLERALTE--- 337

Qy        306 LEGGETPTVGTN 317
              :  :|   |||
Db        338 -DSAQTSDTGTN 348
```

RESULT 14
JC2492
G protein-coupled receptor 1 - rat
N;Alternate names: GPR-1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JC2492
R;Marchese, A.; Cheng, R.; Lee, M.C.; Porter, C.A.; Heiber, M.; Goodman, M.; George, S.R.
Biochem. Biophys. Res. Commun. 205, 1952-1958, 1994
A;Title: Mapping studies of two G protein-coupled receptor genes: An amino acid differenc
A;Reference number: JC2492; MUID:95110347; PMID:7811287
A;Accession: JC2492
A;Molecule type: mRNA
A;Residues: 1-353 <MAR>
A;Cross-references: UNIPROT:P46090; GB:S74702; NID:g786483; PIDN:AAB32978.1; PID:g786484
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester bond; transme
F;74-94/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;134-135/Region: DR motif
F;155-175/Domain: transmembrane #status predicted <TM4>
F;209-229/Domain: transmembrane #status predicted <TM5>
F;246-266/Domain: transmembrane #status predicted <TM6>
F;295-306/Domain: transmembrane #status predicted <TM7>
F;14,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;150,231/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicte
F;330/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match 12.5%; Score 208; DB 2; Length 353;
  Best Local Similarity 24.1%; Pred. No. 1.8e-10;
  Matches 78; Conservative 68; Mismatches 140; Indels 38; Gaps 11;

```
Qy          23 VHTAYLVLSSLAMFTCLCGMAGNSMVIWLLGFRMHRNPFCIYILNLAAADLLFLFSMAST 82
               ||   |:| :||    : |: ||::||| :||:  :    :: |||| || :|:  :
Db          37 VHWISLLLYALAF---VLGIPGNAIVIWFMGFKWKKTVTTLWFLNLAIADFIFVLFLPLY 93

Qy          83 LSLET----QPLVNTTDKVHELMKRLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRP 138
               :|       |      |::  : :|  |:    :  || ||  | : :: |     ||
Db          94 ISYVALSFHWPFGRWLCKLNSFIAQLNMFS---SVFFLTVISLDRYIHLIHPGLSHPHRT 150

Qy         139 RHLSAWVCGLLWTLCLLMNGLTSSF------CSKFLKFNEDRCFRVDMVQ------AALI 186
               |  |   :| |  |: | |  |        :: : :|  : : :::     :
Db         151 LKNSLLVVLFVWLLASLLGGPTLYFRDTVEVNNRIICYNNFQEYELTLMRHHVLTWVKFL 210

Qy         187 MGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFVVVLASVLVFLICSLPLSIYWFVLYW 246
               | | |::|:||  | :  :   |        |: ::|: |: |::|  |  :  | ::
Db         211 FGYLLPLLTMSSCYLCLIFKTKKQNILISSKHLW-MILSVVIAFMVCWTPFHL--FSIWE 267

Qy         247 LSLPPE---MQVL--CFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALR 301
               ||:      ||     ||   : ::|  ||::| ::  :   |    |:  ||:::|
Db         268 LSIHHNSSFQNVLQGGIPLSTGLAFLNSCLNPILYVIISKKFQARF-RASVAEVLKRSLW 326

Qy         302 E-------EPELEGGETPTVGTNE 318
               |       :|   || ::   |
Db         327 EASCSGTVSEQLRSAETKSLSLLE 350
```

RESULT 15
B42009
FMLP-related receptor 1 - human
N;Alternate names: FMLP receptor homolog FPR2; formyl peptide receptor like-1; probable
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
C;Accession: B42009; JC1258; JQ1521; A42492; I54751; S21581
R;Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
Genomics 13, 437-440, 1992
A;Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR),
A;Reference number: A42009; MUID:92307681; PMID:1612600
A;Accession: B42009
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-263,'A',265-338,'C',340-351 <BAO>
A;Cross-references: UNIPROT:P25090; GB:M76672
A;Note: authors translated the codons GTG for residue 15 as Glu, TCT for residue 19 as T
R;Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Andrews, W.H.
Gene 118, 303-304, 1992
A;Title: Cloning of a cDNA encoding a receptor related to the formyl peptide receptor of
A;Reference number: JC1258; MUID:92380523; PMID:1511907
A;Accession: JC1258
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-351 <PER>
A;Cross-references: EMBL:X63819; NID:g31460; PID:g31461
A;Experimental source: bone marrow mRNA
R;Ye, R.D.; Cavanagh, S.L.; Quehenberger, O.; Prossnitz, E.R.; Cochrane, C.G.
Biochem. Biophys. Res. Commun. 184, 582-589, 1992
A;Title: Isolation of a cDNA that encodes a novel granulocyte N-formyl peptide receptor.
A;Reference number: JQ1521; MUID:92246937; PMID:1374236
A;Accession: JQ1521
A;Molecule type: mRNA
A;Residues: 1-351 <YE2>
A;Cross-references: GB:M88107; NID:g189862; PID:g189863
A;Experimental source: granulocytes
A;Note: formyl peptide-stimulated calcium mobilization comparable to that of the formyl
R;Murphy, P.M.; Ozcelik, T.; Kenney, R.T.; Tiffany, H.L.; McDermott, D.; Francke, U.
J. Biol. Chem. 267, 7637-7643, 1992
A;Title: A structural homologue of the N-formyl peptide receptor. Characterization and c
A;Reference number: A42492; MUID:92218423; PMID:1373134
A;Accession: A42492
A;Molecule type: mRNA
A;Residues: 1-351 <MUR>
A;Cross-references: GB:M84562; NID:g182741; PIDN:AAA52473.1; PID:g182742
A;Note: sequence extracted from NCBI backbone (NCBIN:94159, NCBIP:94160)
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993

A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemc
A;Reference number: I54751; MUID:94092629; PMID:7505609
A;Accession: I54751
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-351 <RES>
A;Cross-references: GB:D10922; NID:g219864; PIDN:BAA01720.1; PID:g219865
C;Comment: This G-protein coupled receptor, homologous to the N-formyl peptide receptor f
differentiated myeloid cells and is probably a chemotactic receptor for some other ligand
C;Genetics:
A;Gene: GDB:FPRL1
A;Cross-references: GDB:127554; OMIM:136538
A;Map position: 19q13.3-19q13.4
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein
F;27-53/Domain: transmembrane #status predicted <TM1>
F;59-83/Domain: transmembrane #status predicted <TM2>
F;100-121/Domain: transmembrane #status predicted <TM3>
F;145-169/Domain: transmembrane #status predicted <TM4>
F;206-226/Domain: transmembrane #status predicted <TM5>
F;242-266/Domain: transmembrane #status predicted <TM6>
F;282-307/Domain: transmembrane #status predicted <TM7>
F;4/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;98-176/Disulfide bonds: #status predicted

Query Match 12.4%; Score 206.5; DB 2; Length 351;
Best Local Similarity 25.8%; Pred. No. 2.4e-10;
Matches 92; Conservative 56; Mismatches 126; Indels 83; Gaps 20;

```
Qy          17 YSRGSTVHTAYLVLSSLAM----FTCLCGMAGNSMVIWLLGFRMHRNPFCIYILNLAAAD 72
               |      |  ||  | :      | : :|: || :|||: |||| |    |  |||| ||
Db          12 YEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALAD 71

Qy          73 LLFLFSMASTLSLETQPLVNTTDKVHE------LMKRLMYFAYTVGL----SLLTAISTQ 122
                  ||  :||      | :  :  : |       : :|::    : |     |:  |:
Db          72 ----FSFTATL-----PFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALD 122

Qy         123 RCLSVLFPIWFKCHRPRHLS------AWVCGLLWTLCLLM--------NGLTSSFCSKFL 168
               ||: || |:| : ||    |:       |:  |: || : :          ||   ::|:
Db         123 RCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNG--DTYCT--- 177

Qy         169 KFN--------EDRC-FRVDMVQA----ALIMGVLTP--VMTLSSLTLFVWVRRSSQQWR 213
                ||        |:|    :  |: |     ::|    |  :: :    :   : :
Db         178 -FNFASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKS 236

Qy         214 RQPTRLFVVVLASVLVFLICSLPLSIYWFV-LYWLSLPPEM------QVLCFSLSRLSSS 266
               :| |:   |:||   | ||  |  :   :   ||    ||       :::   ::  ||
Db         237 SRPLRVLTAVVAS---FFICWFPFQLVALLGTVWLK---EMLFYGKYKIIDILVNPTSSL 290

Qy         267 V--SSSANPVIYFLVGSRRSHRLPTRSLGTVLQQALREEPELEGGETPTVGTNEMGA 321
               :|  ||::|  ||      ||   || | |::|| |:          :  ||:  |
Db         291 AFFNSCLNPMLYVFVGQDFRERL-IHSLPTSLERALSED---------SAPTNDTAA 337
```

Search completed: November 4, 2004, 11:02:35
Job time : 42 secs